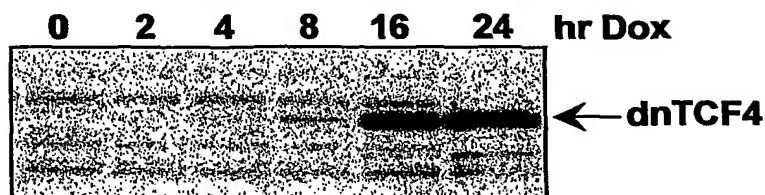
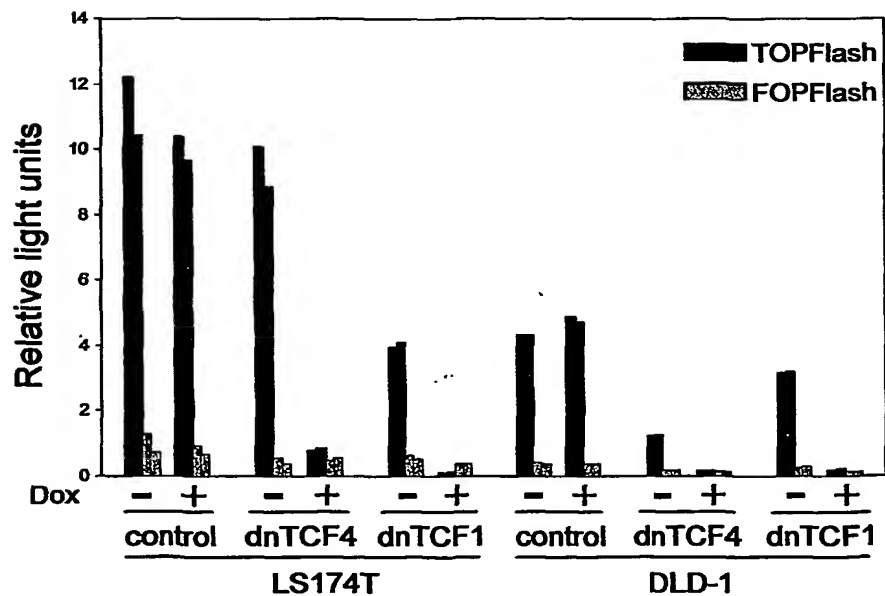
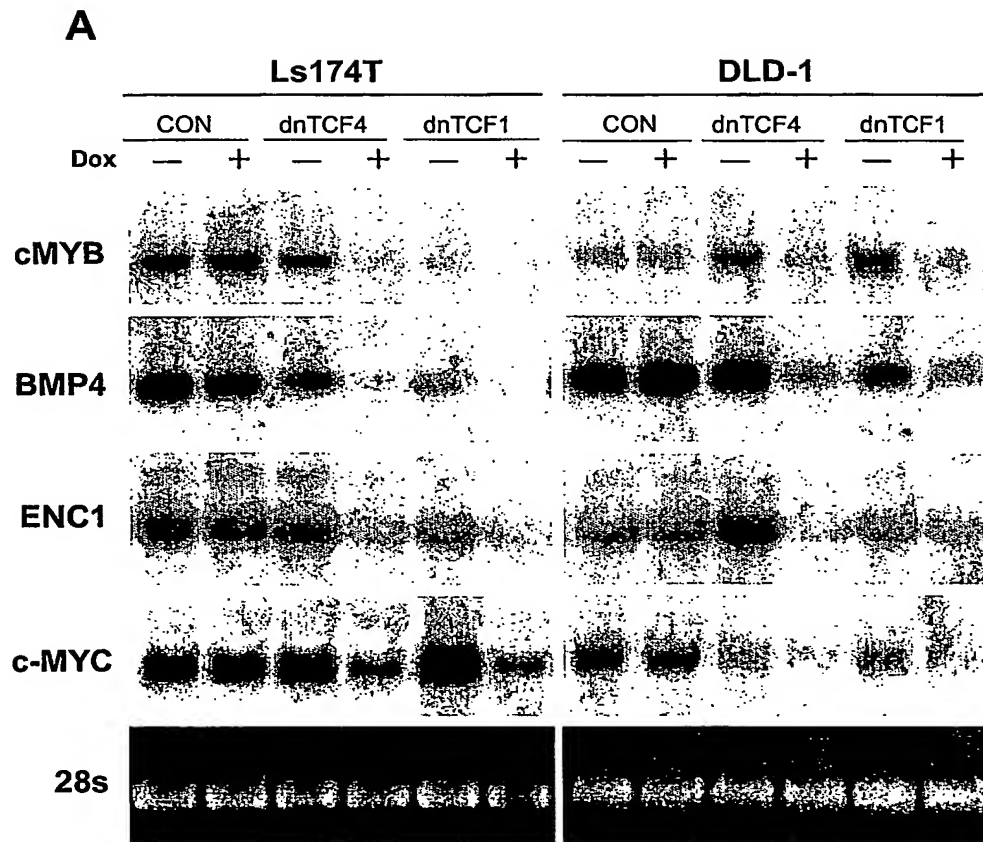
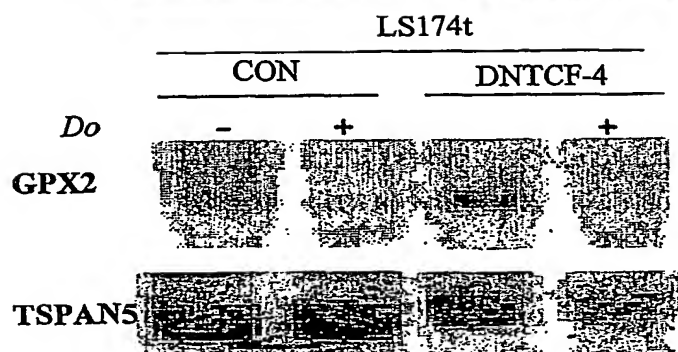
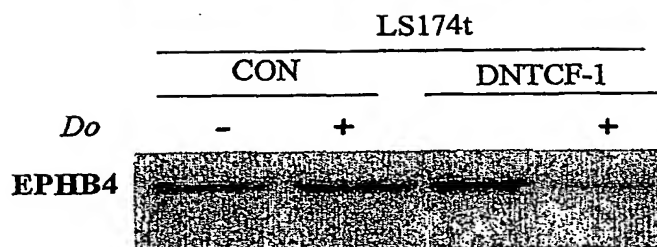
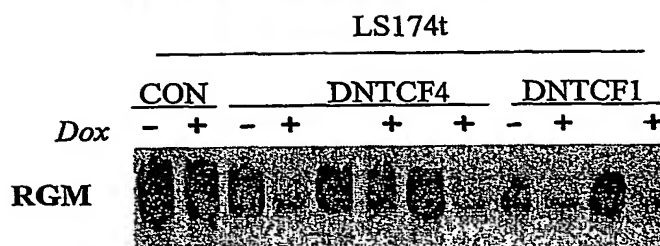
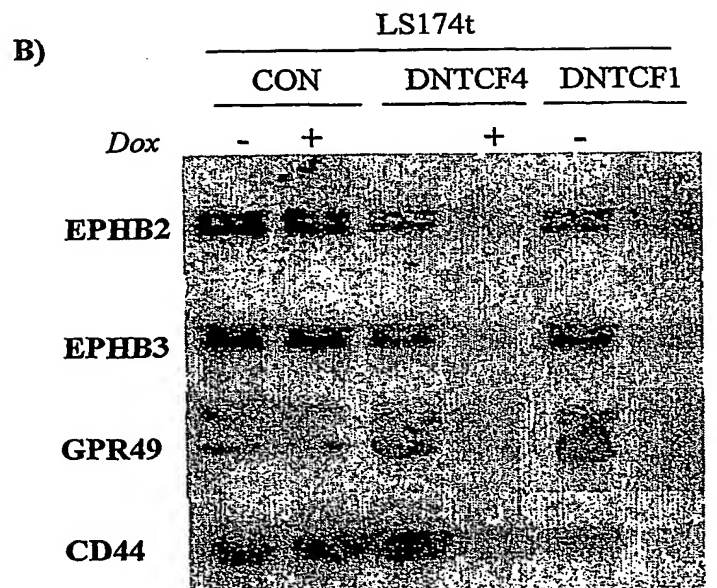
FIG. 1AFIG. 1BFIG. 1C

FIG. 2A



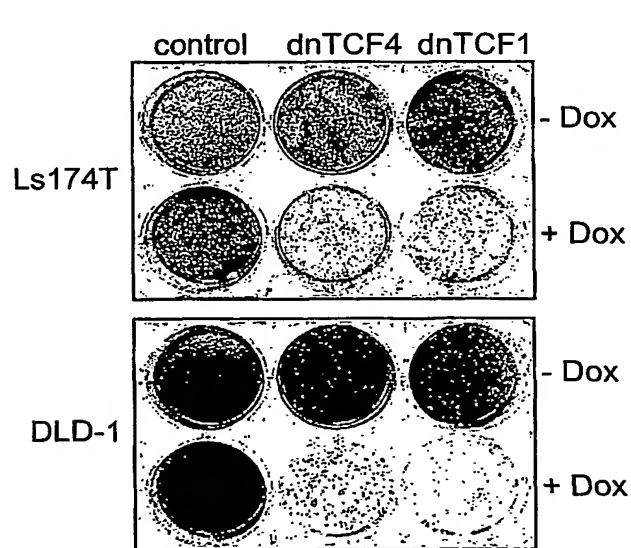
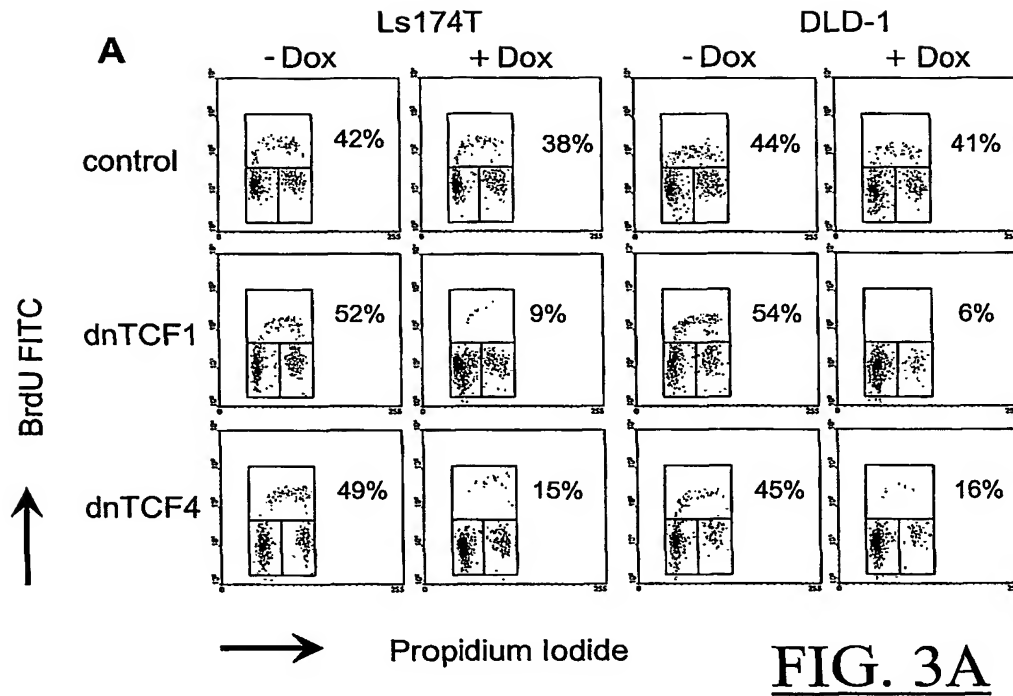


FIG. 3B

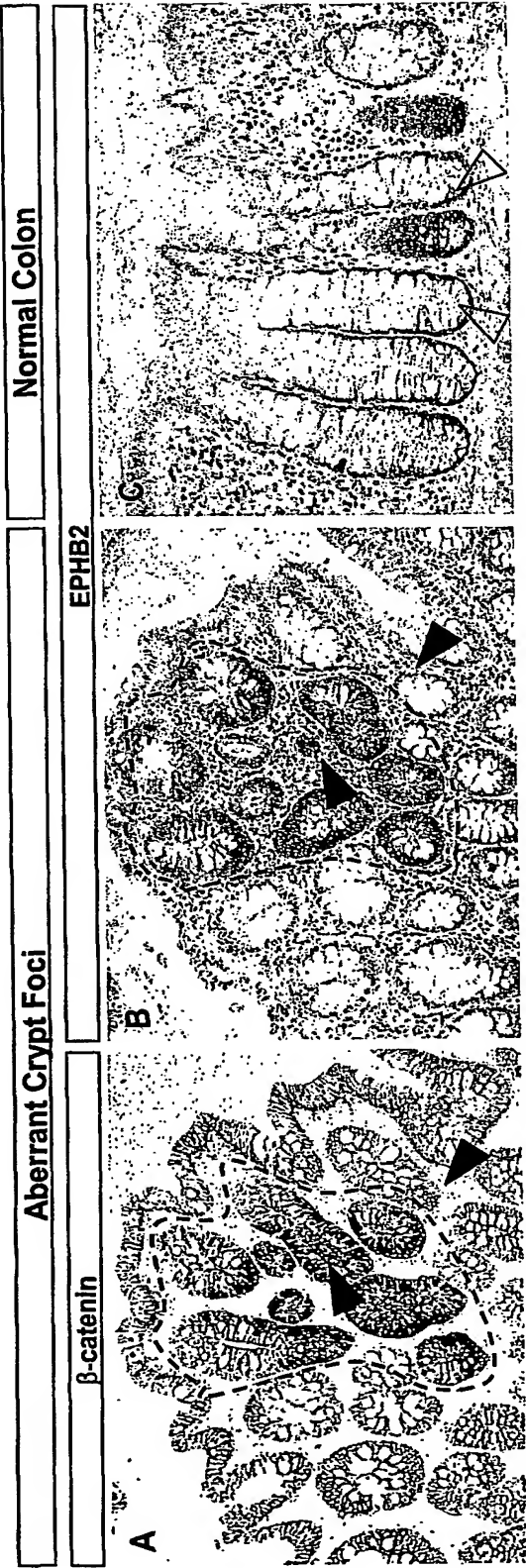


FIG. 4A

FIG. 4B

FIG. 4C



FIG. 5B

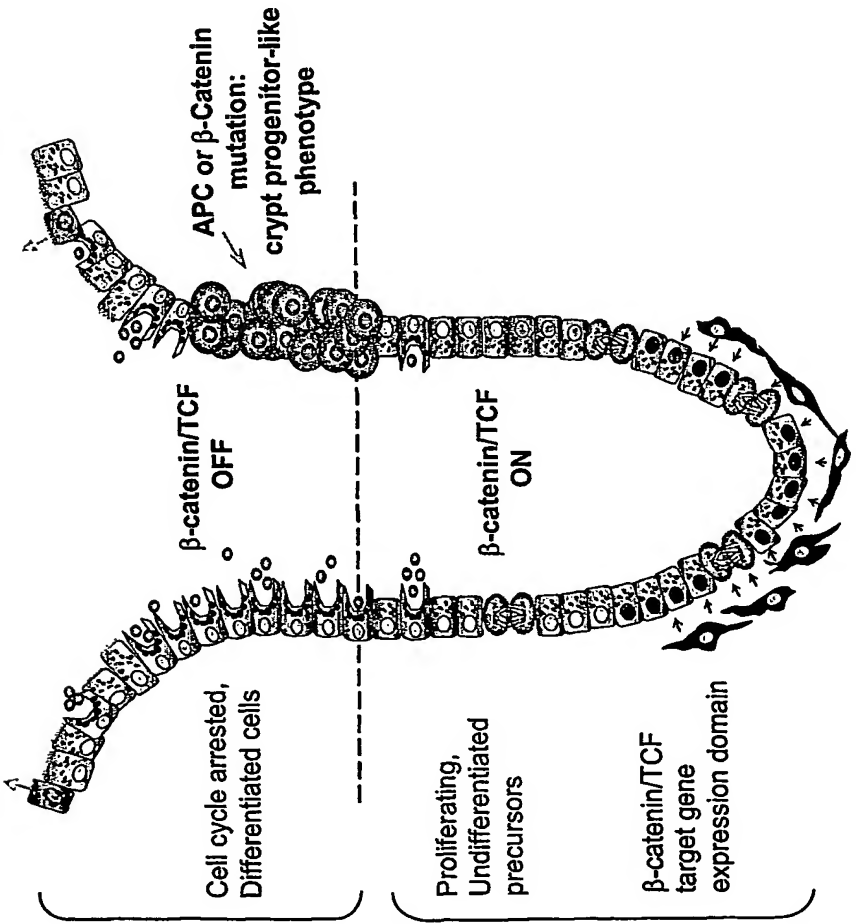


FIG. 5A

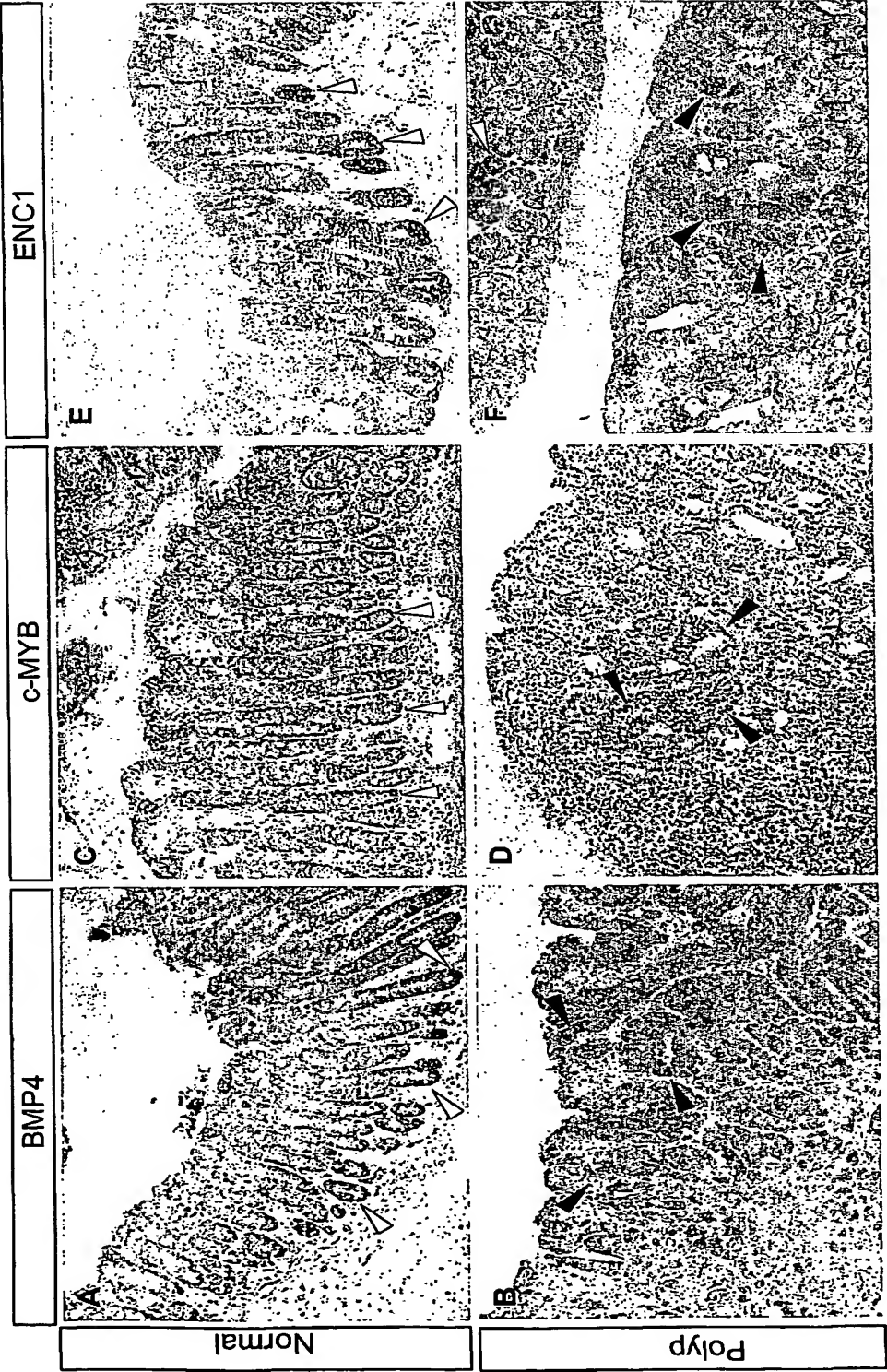


FIG. 6

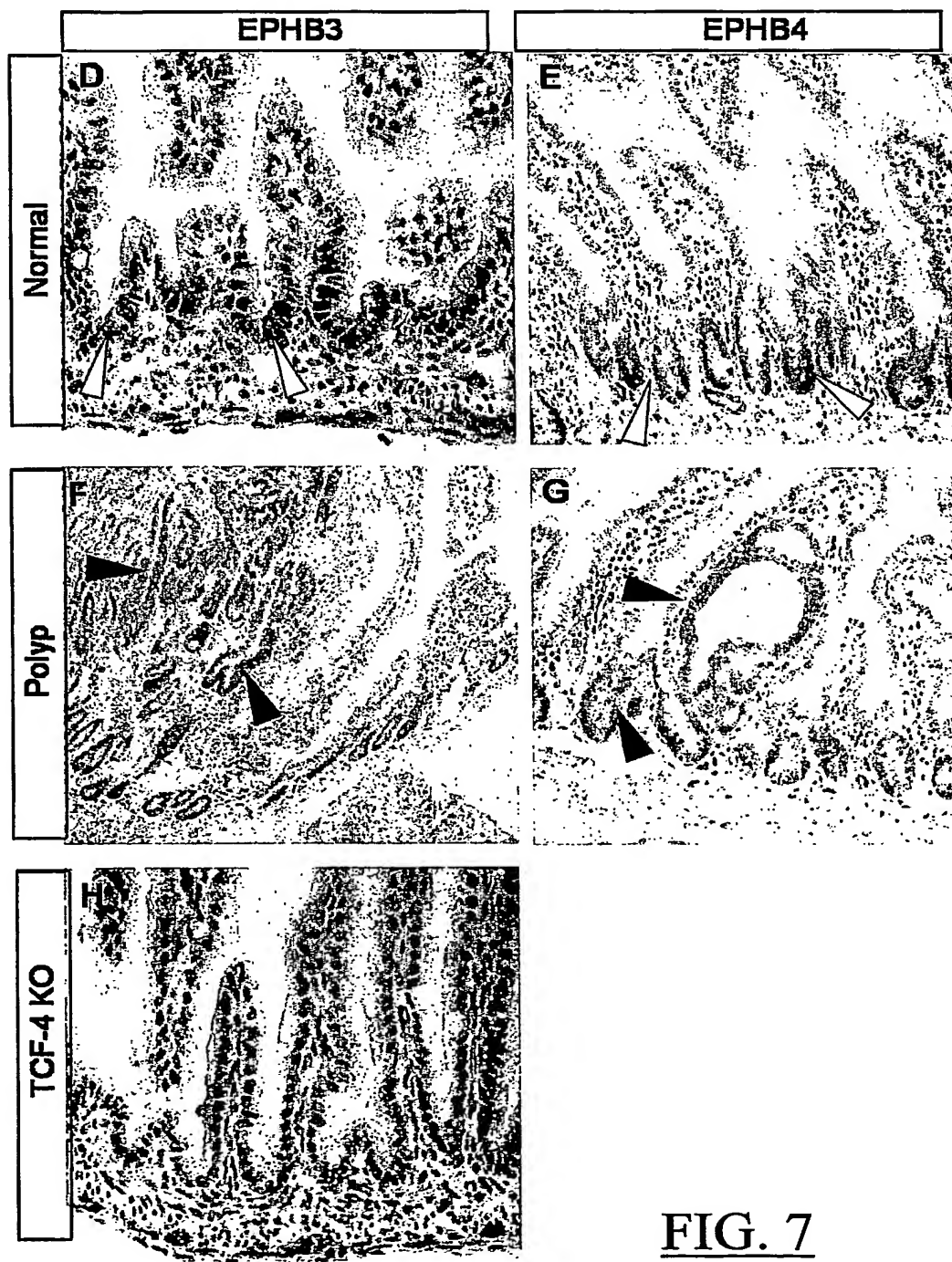


FIG. 7

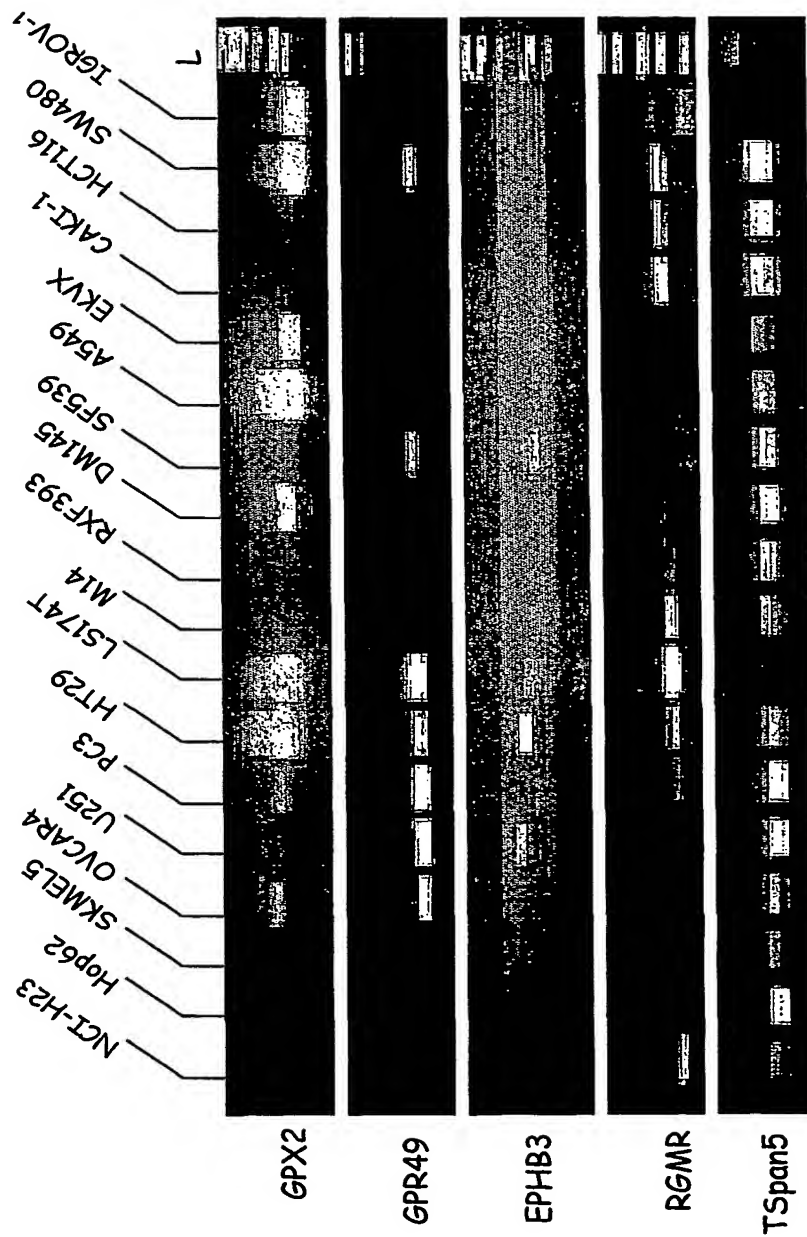
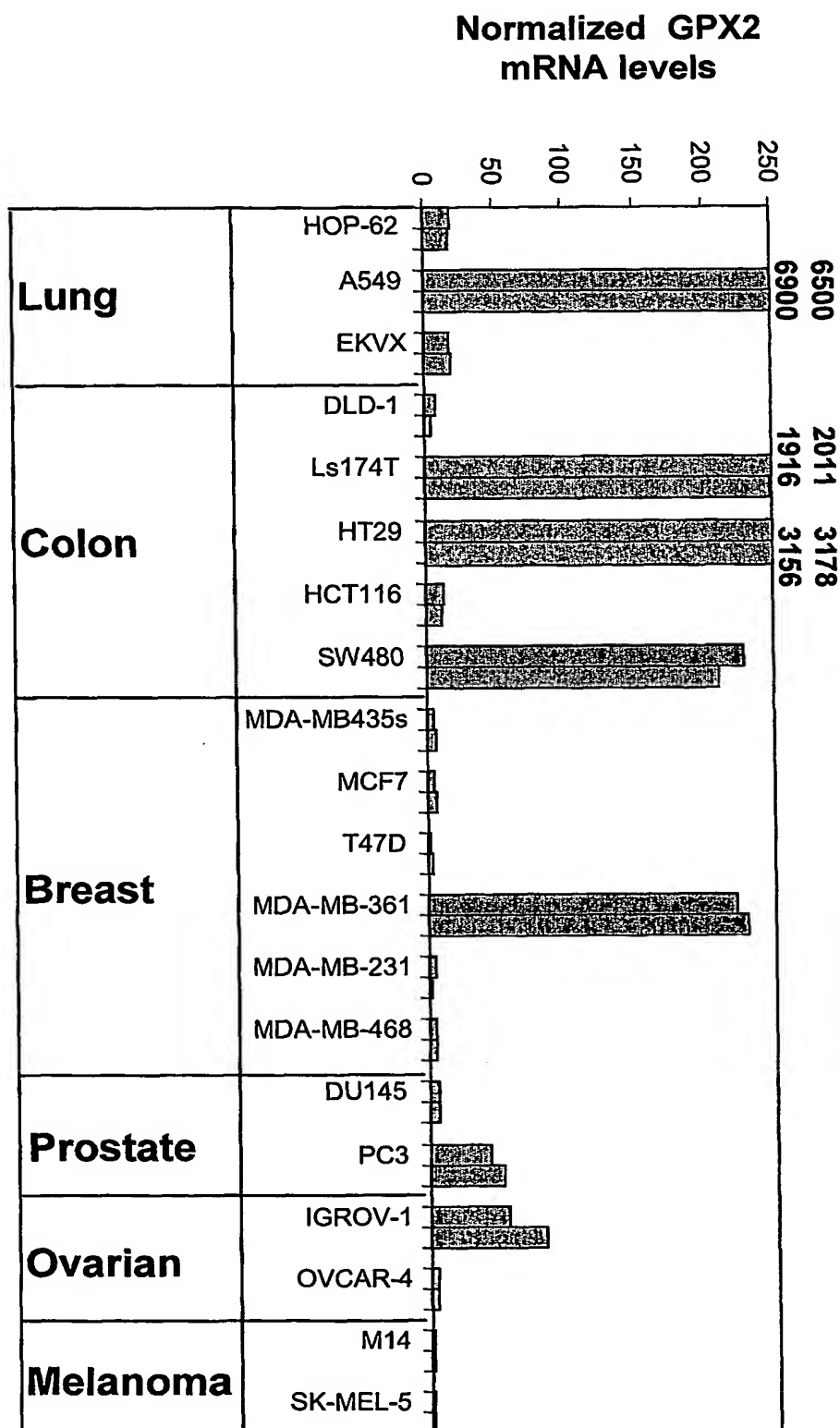
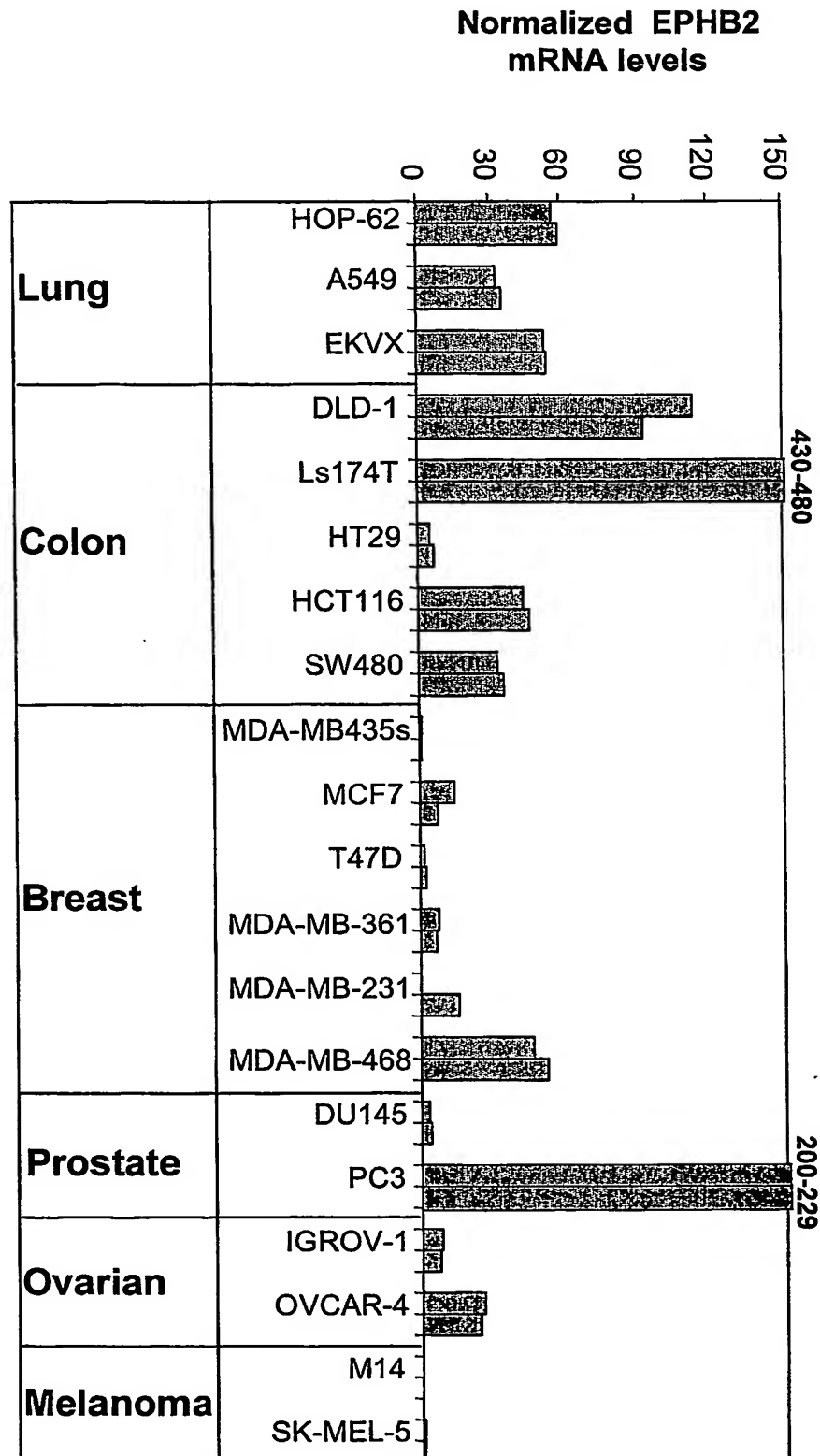


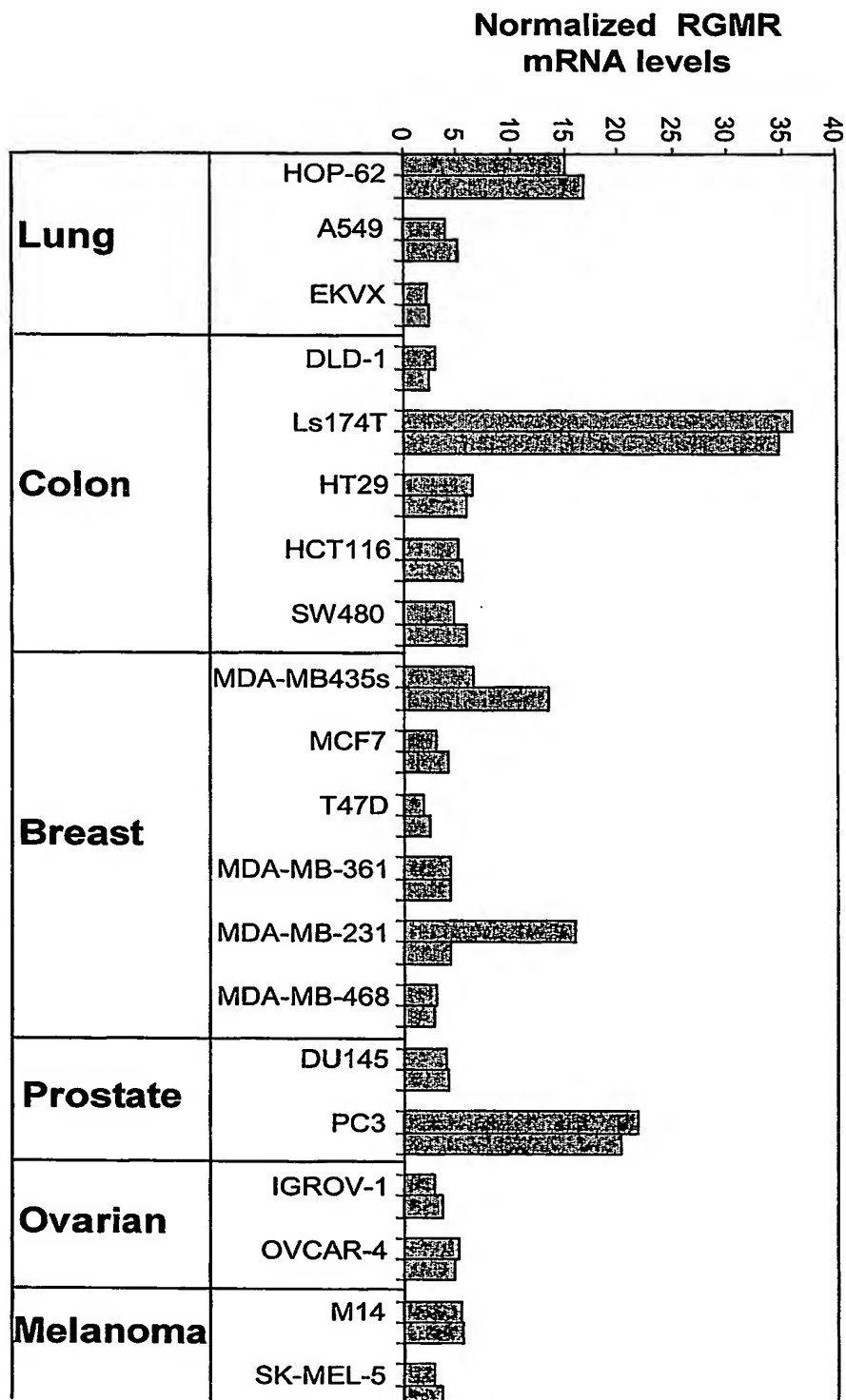
FIG. 8A

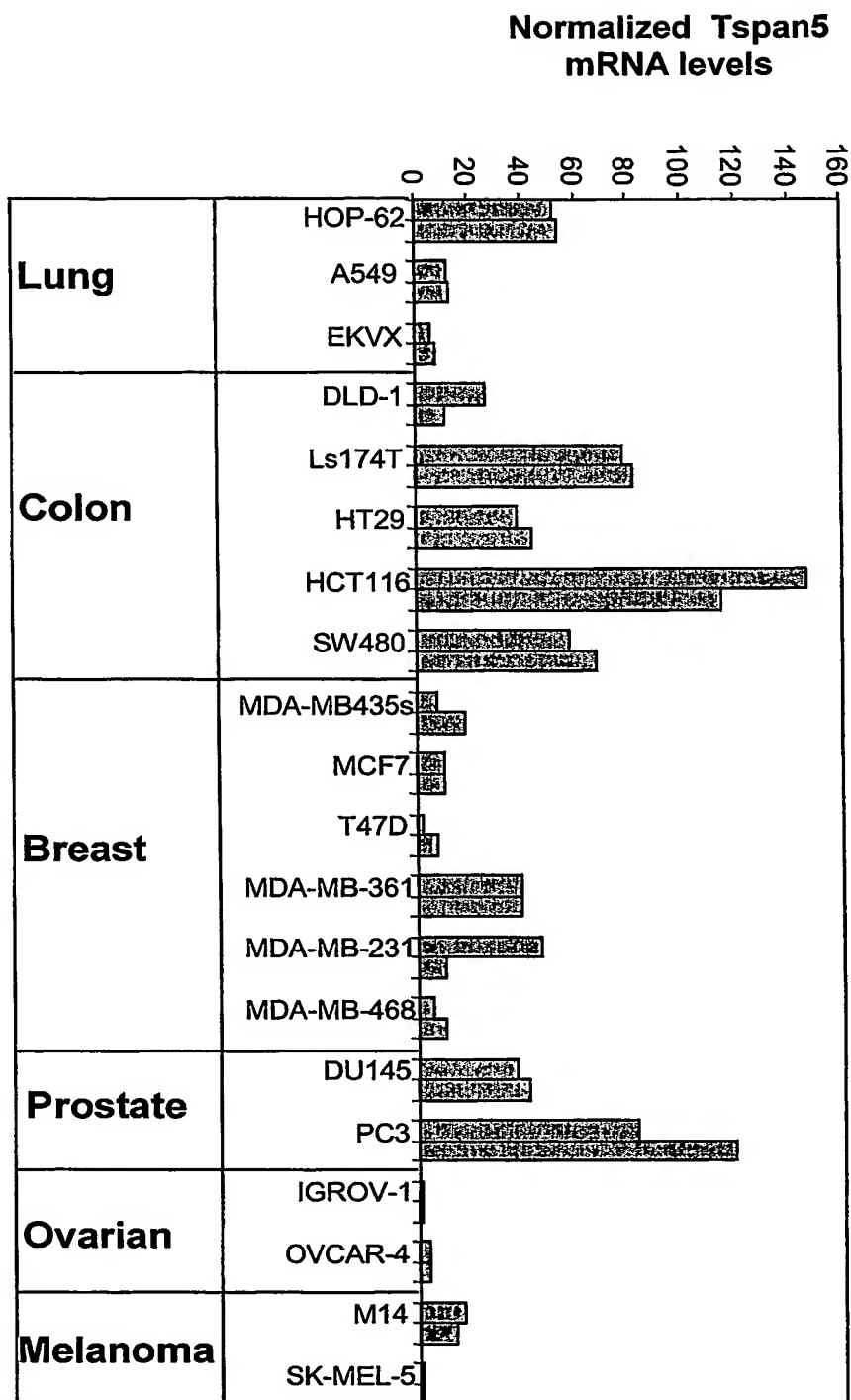
| Cancer Type | Cell-Line | GPX2 Expression Level | GPR49 Expression Level | EPHB3 Expression Level | RGMR Expression Level | TSpan 5 Expression Level |
|------------------------|-----------|-----------------------|------------------------|------------------------|-----------------------|--------------------------|
| Lung | NCL-H23 | + | - | + | ++ | + |
| | Hop62 | + | - | + | + | ++ |
| | A549 | +++ | - | + | + | + |
| | EKVX | +++ | - | + | + | + |
| Ovarian | OVCAR-4 | ++ | ++ | - | + | + |
| | IGROV-1 | +++ | - | - | + | - |
| Central Nervous System | U251 | + | +++ | ++ | + | +++ |
| | SF539 | - | + | ++ | - | ++ |
| Skin | SKMEL5 | - | - | - | + | + |
| | M14 | - | - | + | ++ | + |
| Colon | HT29 | +++ | ++ | +++ | ++ | + |
| | LSI74T | +++ | +++ | ++ | +++ | ND |
| | SW480 | +++ | ++ | - | +++ | +++ |
| | HCT116 | + | - | - | ++ | ++ |
| Prostate | PC3 | ++ | +++ | - | + | +++ |
| | DM145 | +++ | - | - | + | +++ |
| Kidney | RXF393 | - | - | - | + | + |
| | CAKI-1 | - | - | - | +++ | ++ |

FIG. 8B

**FIG. 9A**

**FIG. 9B**

**FIG. 9C**

**FIG. 9D**

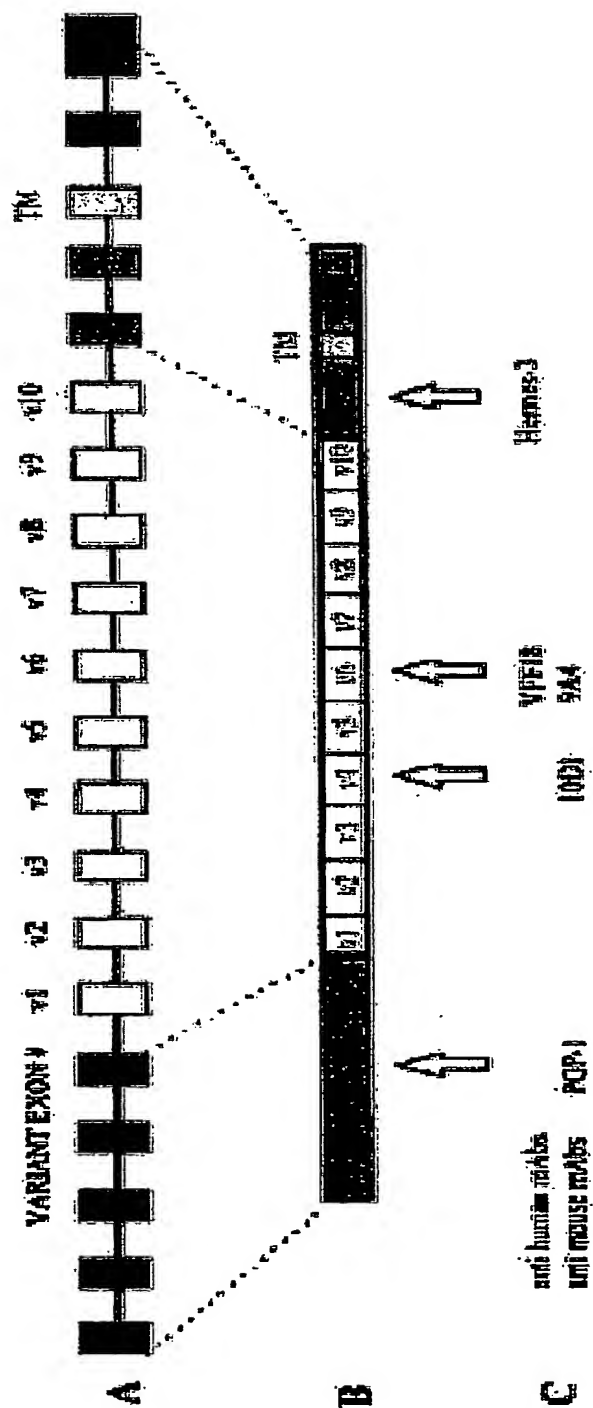


FIG. 10

[illegible]

FIG. 11

Induction
time (hr)

0

24

48

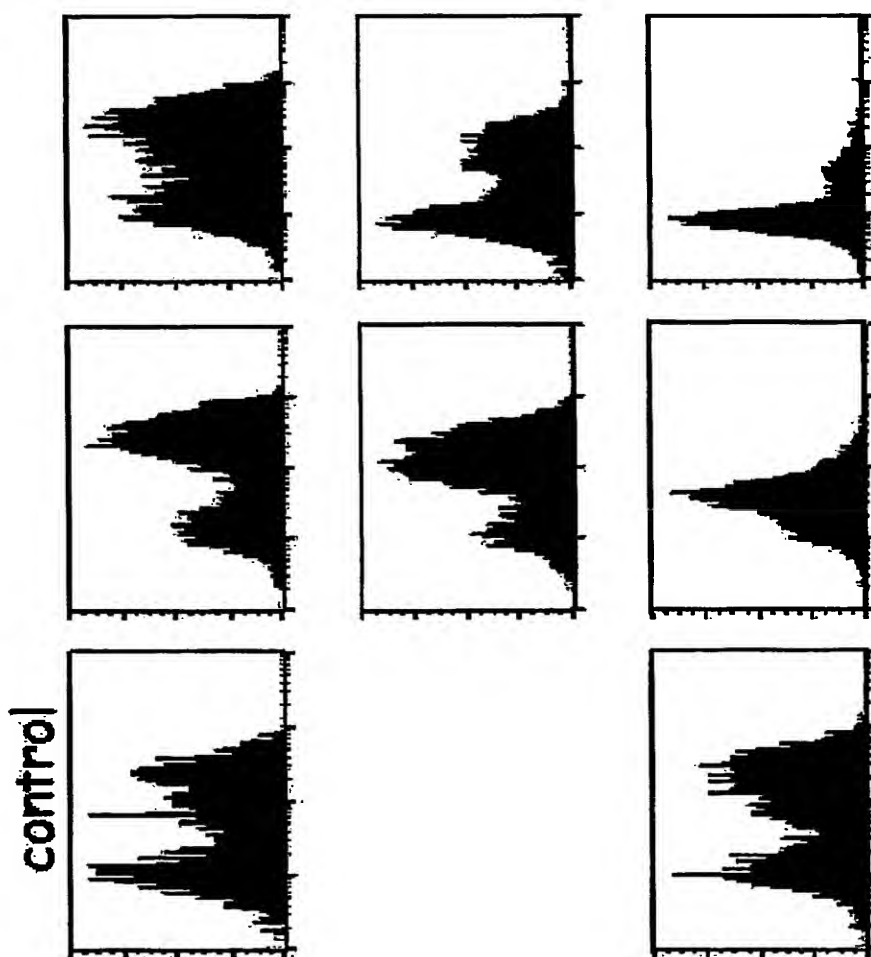


FIG. 12A

Wild-type mouse

TCF-4 KO mouse

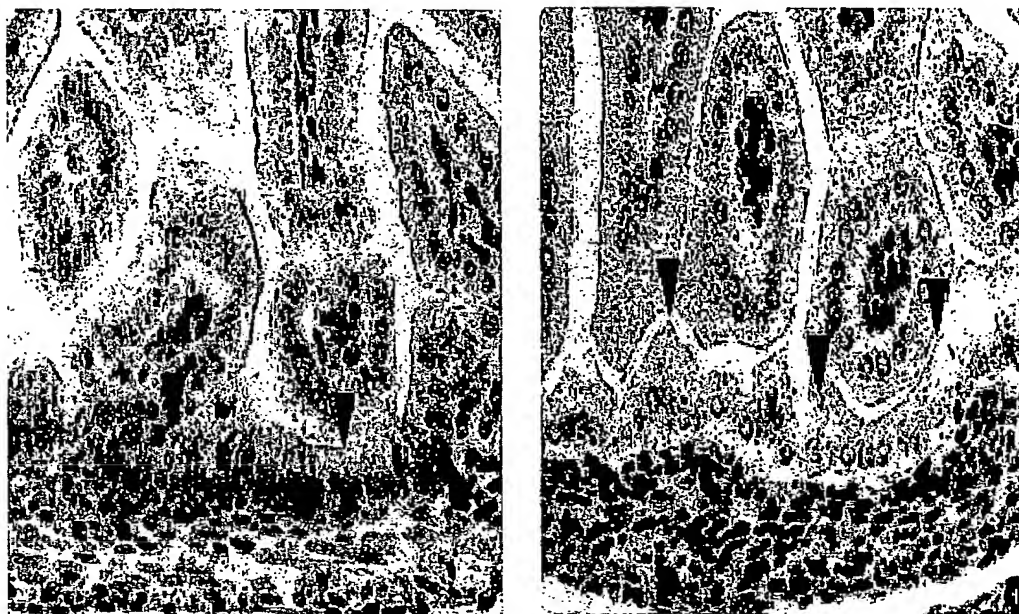


FIG. 12B

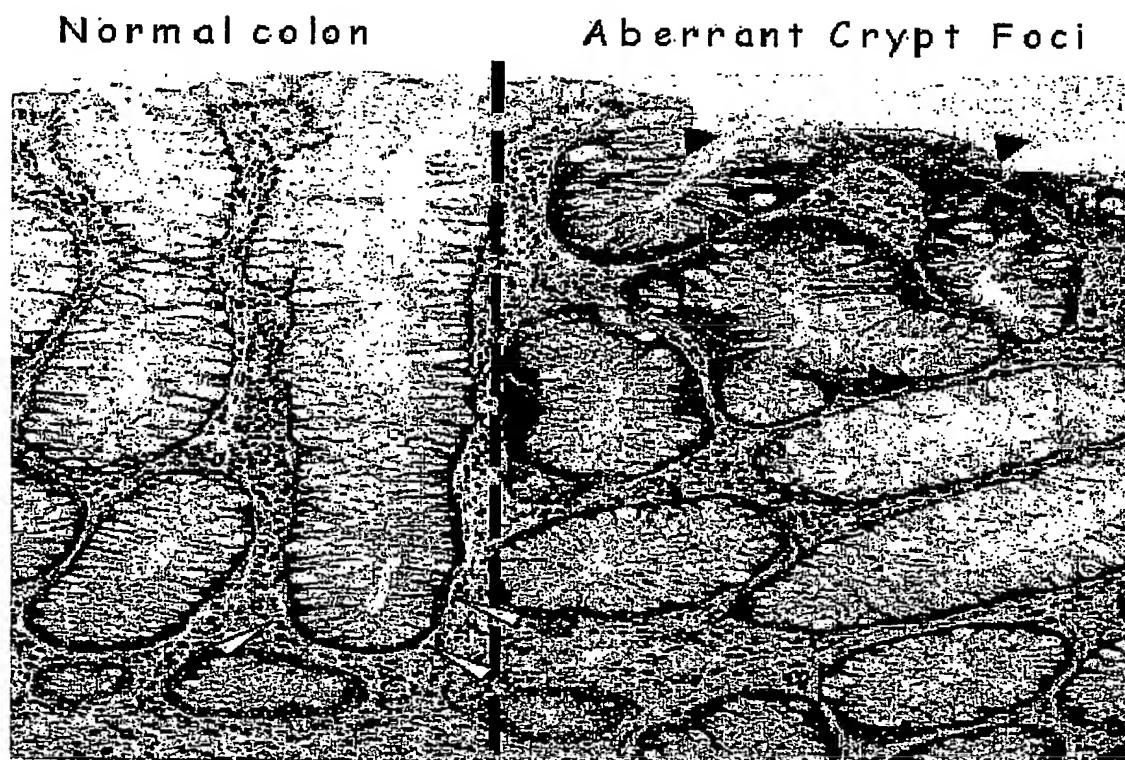


FIG. 13A

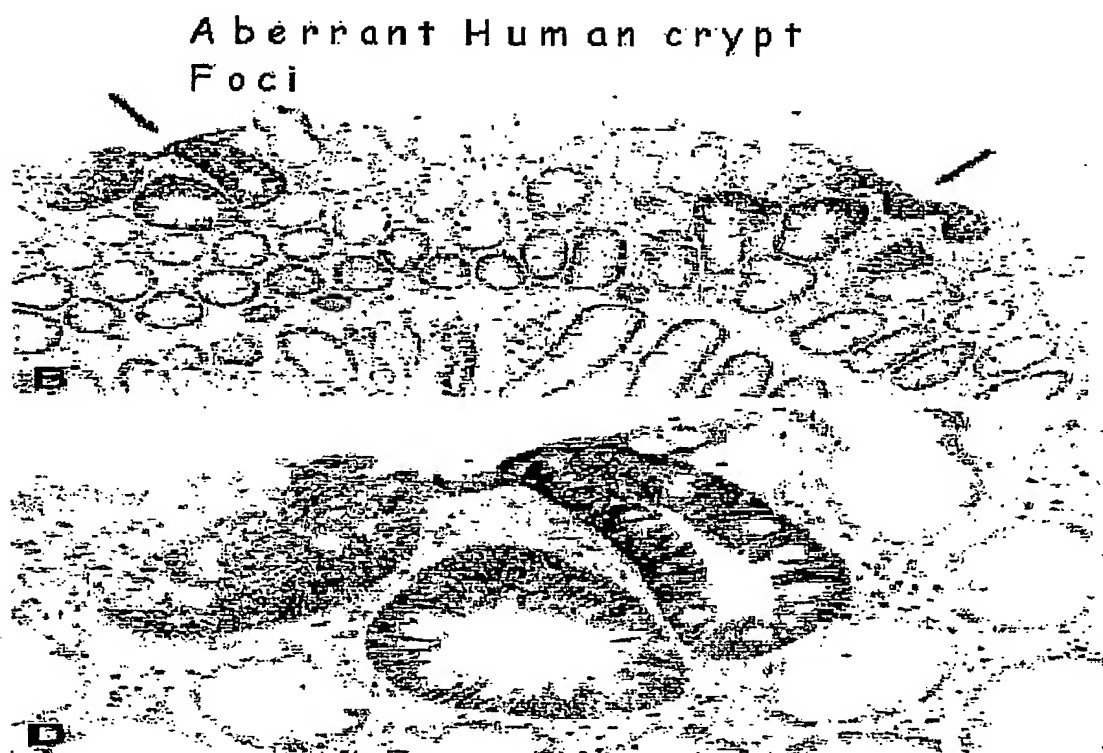


FIG. 13B

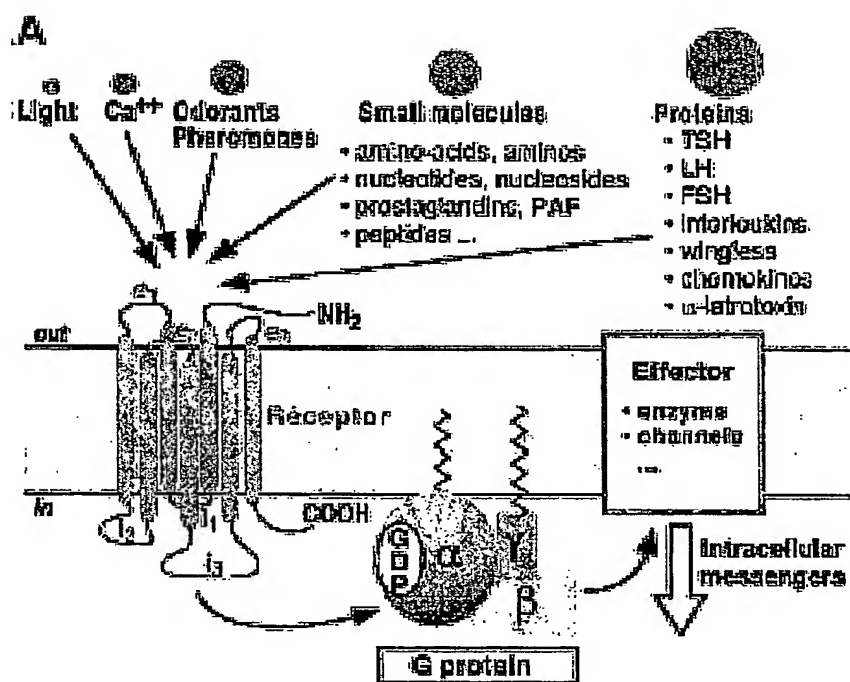


FIG. 14

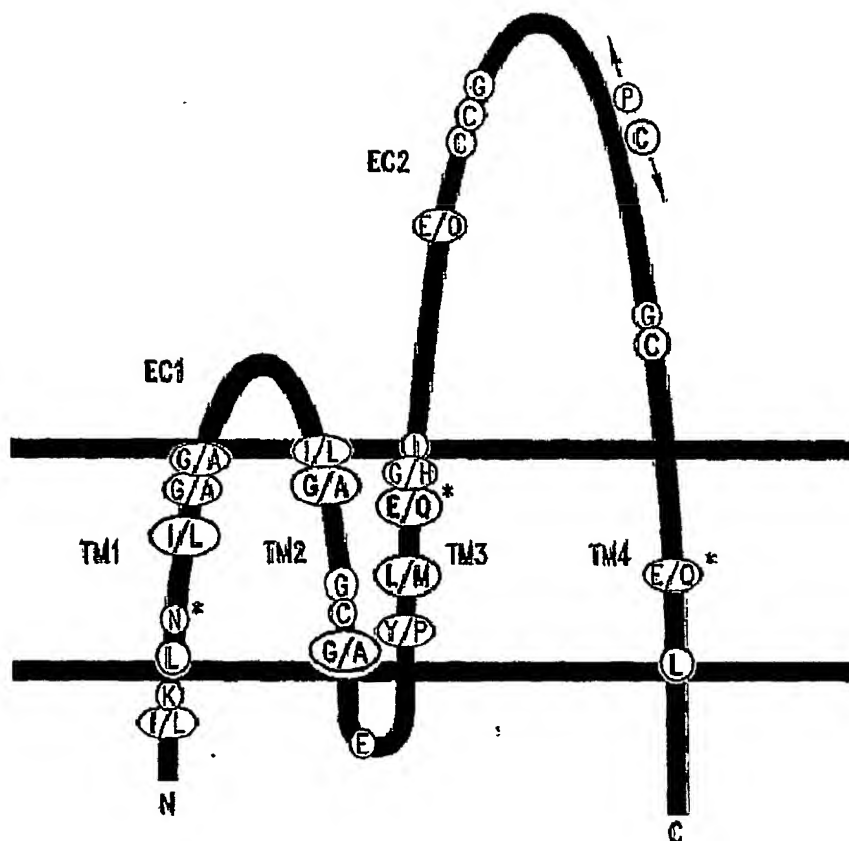
Figure 1 : Lineup of RGM and RGMR Protein Sequences:

| | |
|------------|---|
| humanRGM | --MGRGAG-----RSALGFWP-----TLAFLLLCSFPAATS-----PCK |
| mouseRGM | --MGRGAG-----RSALGLWP-----TLAFLLCSFPAAIS-----PCK |
| chickenRGM | --MGRGAG-----STALGLFQ-----ILPVFLCIFPPVTS-----PCK |
| XenopusRGM | MGMGRGAG-----PKALGEFFK-----ILT VF LCT FHT VSS-----SCK |
| HumanRGMR | --MGLRAAPSSAAAA--AEVEQRRLRPGLCP--FPLELLLLLLL S LG LLH AGDC Q P A OCR |
| mouseRGMR | --MGVRAAPYCAAGPAGAGAESRRPRLPPTPPPPLLLLLL SL G LLH AGDC Q P T QR |
| | * * . : * . : : |
| humanRGM | I L K C N S E F W S A T S - G S H A P A S D D T P E F C A A L R S Y A L C T R T A R T C R G D L A Y H S A V H G I E D |
| mouseRGM | I L K C N S E F W S A T S S G S H A P A S D D V P E F C A A L R T Y A L C T R T A R T C R G D L A Y H S A V H G I E D |
| chickenRGM | I L K C N S E F W A A T S - G S H H L G A E E T P E F C T A L R A Y A H C T R T A R T C R G D L A Y H S A V H G I D D |
| XenopusRGM | I L K C T A D Y L Q A T S N P H H H T G A E D T V E I C T A L R T Y A H C S R T A R T C R G D L A Y H S T V H G I D D |
| HumanRGMR | I Q K C T T D F V S L T S H L N S A V D G F D S - E F C K A L R A Y A G C T Q R T S K A C R G N L V Y H S A V L G I S D |
| mouseRGMR | I Q K C T T D F V A L T A H L N S A A D G F D S - E F C K A L R A Y A G C T Q R T S K A C R G N L V Y H S A V L G I S D |
| | * ** . : : *: . : *: * *** : * **: * : : : * : * . * : * |
| humanRGM | L M S Q H N C S K D G P T S Q P R L R T L P P A G D S Q E R S D S P E I C H Y E K S F H K H S A P N Y T H C G L F G D |
| mouseRGM | L M S Q H N C S K D G P T S Q P R V R T L P P A G D S Q E R S D S P E I C H Y E K S F H K H S A A P N Y T H C G L F G D |
| chickenRGM | L M V Q H N C S K D G P T S Q P R L R T L P P - G D S Q E R S D S P E I C H Y E K S F H K H S A A P N Y T H C G L F G D |
| XenopusRGM | L M S H H N C S K D G P T S Q P R V R I L P P - G D S Q E R S D S P E I C H Y E K S F H R P S A L P N Y T H C G L F G D |
| HumanRGMR | L M S Q R N C S K D G P T S S T N P E V T H D P C N Y H S H A G A R E H R R G D Q -----N P P S Y L F C G L F G D |
| mouseRGMR | L M S Q R N C S K D G P T S S T N P E V T H D P C N Y H S H G V R E H G G G D Q -----R P P N Y L F C G L F G D |
| | ** : : ***** ... : : .. * : : *. ** |
| humanRGM | P H L R T F T D R F Q T C K V Q G A W P L I D N N Y L N V Q A T N T P V L P G S A A T A T S K L T I I F K N F Q E C V D |
| mouseRGM | P H L R T F T D H F Q T C K V Q G A W P L I D N N Y L N V Q V T N T P V L P G S A A T A T S K L T I I F K N F Q E C V D |
| chickenRGM | P H L R T F T D T F Q T C K V Q G A W P L I D N N Y L N V Q V T N T P V L P G S S A T A T S K L T I I F K S F Q E C V E |
| XenopusRGM | P H L R T F S D T F Q T C K I Q G A W P L I D N N Y L N V Q V T N T P V L P G S T A T A T S K L T I I F K N F Q E C V D |
| HumanRGMR | P H L R T F K D N F Q T C K V E G A W P L I D N N Y L S V Q V T N P V V P G S S A T A T N K I T I I F K A H H E C T D |
| mouseRGMR | P H L R T F K D H F Q T C K V E G A W P L I D N N Y L S V Q V T N P V V P G S S A T A T N K V T I I F K A Q H E C T D |
| | *****. * *****: : ******. **. *. *: : *: : *: : *: : * |

FIG. 15A

| | |
|------------|---|
| humanRGM | QKVYQAEMDELPAAFVDGSKNGGDKHGANSKITEKVSQGHVEIQAKYIGTTIVVRQVGR |
| mouseRGM | QKVYQAEMDELPSAFADGSKNGGDKHGANSKITEKVSQGHVEIQAKYIGTTIVVRQVGR |
| chickenRGM | QKVYQAEMDELPAAFADGSKNGGDKHGANSKITEKVSQGHIEIQAKYIGTTIVVRQVGR |
| XenopusRGM | QKVYQAEMDELPAAFIDGSKNGGDKSGANSRLRIEKVSQGHIEIQAKYIGTTIVVRQVGH |
| HumanRGMR | QKVYQAVTDDLPAAFVDGTTSGGD-SDAKSLRIVERESGHYVEMHARYIGTTVFVRQVGR |
| mouseRGMR | QKVYQAVTDDLPAAFVDGTTSGGD-GDVKSLHIVEKESGRYVEMHARYIGTTVFVRQLGR |
| | ***** *:*** ** :..*** ..:*** * : **::*:*:*****:***:* |
| | |
| humanRGM | YLTFAVRMPEEVVNAVEDWDSQGLYLCLRGCPNQQIDFQAFH-TNAEGTGARRLAAASP |
| mouseRGM | YLTFAVRMPEEVVNAVEDRDSQGLYLCLRGCPNQQIDFQAFR-ANAE---SPRRPAAASP |
| chickenRGM | YLTFAVRMPEEVVNAVEDRDSQGLYLCLRGCPNQQIDFQTFRLAQAAEGRARRKGPSLP |
| XenopusRGM | YLTFAVRMPEEVVNAVEDKDNQGLYLCLHGCPCPNQQIDFRNFH-LQAPETGLKRITSASS |
| HumanRGMR | YLTLAIRMPEDLAMS YEE--SQDLQLCVNGCPLSERIDDGQQQVSAILGHSLPRTSLVQA |
| mouseRGMR | YLTLAIRMPEDLAMS YEE--SQDLQLCVNGCPMSECIDDGQQQVSAILGHSLPHTTSVQA |
| | ***:***:.. : * : ..* ** :*** ..: ** : : . |
| | |
| humanRGM | APTAPETFPYETAVAKCKEKL PVEDLYYQACVFDLLTTGDVNFTLAAYYALEDVKMLHSN |
| mouseRGM | SPVVPETFPYETAVAKCKEKL PVEDLYYQACVFDLLTTGDVNFTLAAYYALEDGKMLHSN |
| chickenRGM | AP--PEAFTYESATAKCKEKL PVEDLYYQACVFDLLTTGDVNFTLAAYYAFEDVKMLHSN |
| XenopusRGM | AA----SFTPQTAEAKCKEKL PVKDLYYQACVFDLLTTGDVNFTLAAYYAFEDVKLLHSN |
| HumanRGMR | WP----GYTLETANTQCHEKMPVKDIYFQSCVFDLLTTGDANFTAAAHSALEDVEALHPR |
| mouseRGMR | WP----GYTLETASTQCHEKMPVKDIYFQSCVFDLLTTGDANFTAAAHSALEDVEALHPR |
| | . :. :* :*:***:***:***:*****.* ** : ** : **.. |
| | |
| humanRGM | KDKLHLYERTRDLPGRAAAG-----LPLAPRPLL GALVPLLALLPVFC--- |
| mouseRGM | KDKLHLFERTRELPGAVAAAAAATTFPLAPQILG-TIPLLVLPLVW--- |
| chickenRGM | KDKLHLYERTRALAPGNAAP-----SEHPWALPALWVALLSLSQCWLGLL |
| XenopusRGM | KNKVHLFERP----- |
| HumanRGMR | KERWHIFPSSGNGTP-----RGGSDLVSLGLTCLILIVFL--- |
| mouseRGMR | KERWHIFPSSCG-----GCRDLPVGLGLTCLILIMFL--- |
| | *: * : . |

FIG. 15B

FIG. 16

ATGGACAAGTTTTGGTGGCAGCAGCCTGGGGACTCTGCCTCGTGCCGCTGAGCCTGGCGCAGATCGATTTGAATATAACCTGCCG
CTTTGCAGGTGTATTCCACGTGGAGAAAAATGGTCGTACAGCATCTCTCGGACGGAGGCCGCTGACCTCTGCAAGGCTTTCAATA
GCACCTTGCCCAATGGCCAGATGGAGAAAGCTCTGAGCATCGGATTTGAGACCTGCAGGTATGGGTTTATAGAAGGGCAGCTG
GTGATCCCCGGATCCACCCCACTCCATCTGTGCAGCAAAACACAGGGGTGTACATCCTCACATCCAACACCTCCAGTATGA
CACATATTGCTTCAATGCTTCAGCTCCACCTGAAGAAGATTGTACATCAGTCACAGACCTGCCCAATGCCCTTGATGGACCAATTA
CCATAACTATTGTTAACCGTGATGGCACCCTGATGTCCAGAAAGGAGAAATACAGAACGAATCCTGAAGACATCTACCCAGCAAC
CCTACTGATGATGACGTGAGCAGCGGCTCCTCCAGTGAAGGAGCAGCACTTCAGGAGGTACATCTTTTACACCTTTCTACTGT
ACACCCCATCCAGACGAAGACAGTCCCTGGATCACCAGACAGCAGACAGAATCCCTGCTACCCTTTGATGAGCACTAGTGCTA
CAGCAACTGAGACAGCAACCAAGAGGCAAGAAACCTGGGATTGGTTTTTCATGGTTGTTTCTACCATCAGAGTCAAAAGAATCATCTT
CACACAACACACAATGGCTGGTACGTCTTCAAATACCATCTCAGCAGGCTGGGAGCCAAATGAAGAAAATGAAGATGAAGAGA
CAGACACCTCAGTTTTCTGGATCAGGCATTGATGATGATGAAGATTTTATCTCCAGCACCATTTCACACACACCGGGCTTTTG
ACCACACAAAACAGAACAGGACTGGACCCAGTGGAACCCAAAGCCATTCAAATCCGGAAGTGCTACTTCAGACAACCAAGGATG
ACTGATGTAGACAGAAATGGCACCCTGCTTATGAAGGAACTGGAACCCAGAAAGCACACCCCTCCCTCATTACCATGAGCATCA
TGAGGAAGAAGAGACCCACATTCTACAAGCACAATCCAGGCAACTCCTAGTAGTACAACGGAAGAAACAGCTACCCAGAGGAAG
AGTGGTTTTGGCAACAGATGGCATGAGGATATCGCCAAACACAGCAAGAACTCCCATTCGACAACAGGACACTCAGATGGGATCA
GCTCATACCAGCCATCCAATGCAAGGAAGGACAACCAAGCCAGAGGACAGTTCCTGGACTGATTTCTTCAACCAATCTCACA
CCCCATGGGACGAGGTCTCAAGCAGGAAGAAGGATGGATATGGACTCCAGTCAATAGTATAACGCTTCAGCCTACTGCAAAATCCAA
ACACAGGTTTGGTGGAGATTGGACAGGACAGGACCTCTTCAATGACAACGAGCAGAGTAATCTCAGAGCTTCTCTACATCA
CATGAAGGCTTGGAAAGATAAAGACCATCCAACAACCTCTACTCTGACATCAAGCAATAGGAATGTACAGGTGGAAGAAAG
AGACCCAAATCATTCTGAAGGCTCAACTACTTTACTGGAAGGTATACCTCTCATTACCCACACAGGAAGGAAGCAGGACCTTCA
TCCCACTGACCTCAGCTAAGACTGGGTCTTTGGAGTTACTGCAGTTACTGTTGGAGATTCCAACCTCAATGTCAATCGTTCTCTTA
TCAGGAGACCAAGACACATTTCCACCCAGTGGGGGGTCCCATACCACCTCATGGATCTGAATCAGATGGACACTCAGATGGGATCA
AGAAGGTGGAGCAACACAACCTCTGGTCTATAAGGACACCCCAATTCAGAAATGGCTGATCATCTTGGCATCCCTCTTGGCCT
TGGCTTTGATTCTTGCAGTTTGCATTGCAGTCAACAGTGAAGAAGGTGTGGGAGAGAAAAGCTAGTGATCAACAGTGGCAAT
GGAGCTGTGGAGGACAGAAAGCCAAAGTGGACTCAACGGAGAGGCCAGCAAGTCTCAGGAATGGTGCAATTTGGTGAACAAGGAGTC
GTCAGAACTCCAGACCAGTTTATGACAGCTGATGAGACAAGGAACCTGCAGAAATGTGGACATGAAGATTGGGGTGAACACCTAC
ACCATTATCTTGGAAAGAAACAACCGTTGGAAACATAACCATTACAGGAGCTGGGACACTTAACAGATGCATGTGCTACTGATT
GTTTCATTGCGAATCTTTTTAGCATAAAATTTTCTACTCTTTTTGTTTTTGTGTTTTGTTCTTTAAAGTCAGGTCCAATTTGTA
AAAACAGCATTTGCTTTCTGAAATTAGGGCCCAATTAATAACACAGCAAGAATTTGATCGTTCCAGTTCACCTTGGAGGCCCTTCAT
CCCTCGGGTGTGCTATGGATGGCTTCTAACAAAACACTACACATATGTATTCTGATCGCCAACTTTCCCCCACCAGCTAAGGACA
TTTCCCAAGGTTAATAGGGCTGGTCCCTGGGAGGAAATTTGAATGGGTCCATTTGCCCCCTCATAGCCTAATCCCTGGGCATTG
CTTTCCACTGAGGTTGGGGGTGGGGGTGTACTAGTTACACATCTTCAACAGACCCCTCTAGAAATTTTTCAGATGCTTCTGGGAG
ACACCCAAAGGGTGAAGCTATTTATCTGTAGTAACTATTTATCTGTGTTTTTGAATATTAACACCTGGATCAGCTCTTTGATCA
GTATAATTTTTTAAAGTTACTTTGTCTAGAGGCACAAAAGGGTTTAAACTGATTATAATAATATCTGTACTTCTTGATCTTCAC
CTTTTGTGCTGTGATTCTTCAAGTTTCTAAACAGCAGCTGTCTGGTCCCTACAATGTATCAGGAAGAGCTGAGAATGGTAAGGAGA
CTCTTCTAAGCTCTTCACTCAGAGACCTGAGTTCCTCAGACCCCTCAGCCAAATCTCATGGAAAGCAAGGAGGCGAGCAC
TGTTTTTGTTTTTTGTTTTTTGTTTTTTTTTTGACACTGTCCAAGGTTTTCCATCCTGTCTTGAATCAGAGTTGGAAGCTGA
GGAGCTTCAGCCTCTTTTATGGTTTAAATGGCCACCTGTTCTCTCTGTGAAAGGCTTTGCAAAAGTCACTTAAGTTTGCATGACCT
GTTATCCCTGGGGCTTATTTATAGAGGCTGGCCCTATTAGTATGTTTTTCAAAAACAATATGGAAGTGCCTTTTGTGCTTTACAA
TAAGAGAAGAAGCCAAATGGAATGAAGAGATTGGCAAGGGGAAGGATGATGCCATGTAGATCCTGTTTGTAGATCTTTTGTGCTG
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TTAAAGGGATTCCCATCATTTGAATCTTATCACCAGATAGGCAAGTTTATGACCAACAAGAGAGTACTGGCTTTATCCTCTAAC
TCATATTTTCTCCCACTTGGCAAGTCTTTGTGGCATTATTATCAGTCAGGCTGTCCGATTGGTCCCTAGAACTTCAAAGGCTG
CTTGTCTAGAGAAGCATTGCACTCTATAAAGCAACGGCTCCTGTAAATGGTATCTCCTTTCTGAGGCTCCTACTAAAAGTCATTG
TTACCTAACTTATGTGCTTAAACAGGCAATGCTTCTCAGACCACAAAGCAGAAAGAAGAAAGCTCCTGACTAAATCAGGGCT
GGGCTTAGACAGAGTTGATCTGTAGAATATCTTAAAGGAGAGATGCAACTTTCTGCACTATTCCAGCCTGTGCTCCTCCTGT
CTACCTCTCCCCCTCCTCCTCCTCCACTTCAACCCACAATCTTGA AAAACTTCTTTCTCTCTGTGAACATCATTTGGCCAGA
TCCATTTTCAGTGGTCTGGATTTCTTTTATTTTCTTTTCAACTTGAAGAACTGGACATTAGGCCACTATGTGTTGTTACTGCC
ACTAGTGTCAAGTGCTCTTGTTTTCCAGAGATTCTCTGGTCTGCCAGAGGCCAGACAGGCTCACTCAAGCTCTTAACTGA
AAGCAACAAGCCACTCCAGGACAAGGTTCAAATGGTTACACAGCCTCCTACCTGTGCGCCCAAGGAGAAAGGGGTAGTGATACA
AGTCTCATAGCCAGAGATGGTTTTCCACTCCTCTAGATATTCCCAAAAAGAGGCTGAGACAGGAGGTTATTTCAATTTTATTTT
GGAATTAATAACTTTTTTCCCTTTATTTACTGTTGTAGTCCCTCACTTGGATATACCTCTGTTTTACAGATGAATAAGGGAGGTC
TAGAGCTTCTATTCTTTGGCCATTGTCAACGGAGAGCTGGCCAGTCTTCACAAACCTTGCAACATTCGAGAGTTTATGGAGT
AAGATGTATCTCACTCCCTTGATCTCAAGGGCGTAACCTGGAAGCACAGCTTGACTACACGTCAATTTTACCAATGATTTTTCAG
GTGACCTGGGCTAAGTCATTTAACTGGGCTTTATAAAGTAAAAGGCCAACATTTAATTTATTTGCAAGCAACCTAAGAGCTA
AAGATGTAATTTTTCTTGAATTTGTAATCTTTTGTGTCCTGTAAGACTTCCCTTAAATTAGCTCTGAGTGA AAAATCAAAGG
GACAAAAGACATCTTCAATCCATATTTCAAGCCTGGTAGAATTTGGCTTTTCTAGCAGAACCTTTCCAAAGTTTATTTGAGAT
TCATAACACACCAAGAAATGATTTTGTAGCCAACATTCATTCAATCTGTTATATCAGAGGAGTAGGAGAGAGGAACATTTGAC
TTATCTGGA AAAAGCAAAATGACTTAAAGATAAGAAATAACATGGTCCATTTACCTTTATGTTATAGATATGTCTTTGTGTAATCA
TTGTTTTGAGTTTTTCAAAGAAATAGCCATTGTCTCTGTTGTAACAATGACCAGTGTATTTGTTACTTTTTCAGAG
CACACCTTCTCTGTTTTTGTATATTTATTTGATGGATCAATAATAATGAGGAAGCATGATATGTATATTGCTGAGTTGAAAGC
ACTTATTGGA AAAATATTAAGGCTAACATTAAGAGCTAAAGGAAAACAGACTCAGA

(SEQ ID No. 1)

FIG. 17A

SUBSTITUTE SHEET (RULE 26)

MDKFWWHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFETCR
YGFIEGHVVIPRIHPNSICAANNTGVYILTSNTSQYDITYCFNASAPPEEDCTSVTDLPNAFDGPITITIVNRDGYVQKGE
YRTNPEDIYPSNPTDDDVSSGSSERSSTSGGYIFYTFSTVHPIPEDDSPWITDSTDRIPTATLMSTSATATETATKRQETW
DWFSWFLPSESKNHLHTTTQMAGTSSNTISAGWEPNEENEDERDRHLSFSGSGIDDEDFFISSTISTTPRAFDHTKQNQ
DWTQWNPSHSNPEVLLQTTTRMTDVDRNGTTAYEGNWNPEAHPPLIHHEHHEEEETPHSTSTIQATPSSSTEETATQKE
QWFGNRWHEGYRQTPREDSSHSTGTAAASAHTSHPMQGRTPSPEDSSWTDFFNPISHPMGRGHQAGRMDMDSSHSI
TLQPTANPNTGLVEDLDRTGPLSMTTQQSNSQSFSSTHEGLEEDKDHPPTTSTLTSSNRNDVTGGRRDPNHSEGSTTLLEG
YTSHYPHTKESRTFIPVTSAKTGSFGVTA VTVGDSNSNVNRSLSGDQDTFHPSGGSHHTHGSESDGHSQEGGANTT
SGPIRTPQIPEWLILASLLALALILAVCIAVNSRRRCGQKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSE
TPDQFMTADETRNLQNVDKIGV*

(SEQ ID No. 2)

FIG. 17B

ATGGACAAGTTTGGTGGCACGCAGCCTGGGGACTCTGCCTCGTGCCGCTGAGCCTGGCGCAGATCGATTTGAATATAACCTGCCG
CTTTGCAGGTGTATTCCACGTGGAGAAAAATGGTCGCTACAGCATCTCTCGGACGGAGGCCGCTGACCTCTGCAAGGCTTTCAATA
GCACCTTGCCCACAATGGCCCAGATGGAGAAAGCTCTGAGCATCGGATTGAGACCTGCAGGTATGGGTTTCATAGAAGGGCATGTG
GTGATTCCCGGATCCACCCCACTCCATCTGTGCAGCAAACAACACAGGGGTGTACATCCTCACATAACAACCTCCAGTATGA
CACATATTGCTTCAATGCTTCAGCTCCACCTGAAGAAGATTGTACATCAGTCACAGACCTGCCAATGCCTTTGATGGACCAATTA
CCATAACTATGTGTTAACCGTGATGGCACCCGCTATGTCCAGAAAGGAGAATACAGAACGAATCCTGAAGACATCTACCCAGCAAC
CCTACTGATGATGACGTGAGCAGCGGCTCCTCCAGTGAAGGAGCAGCACTTCAGGAGGTTACATCTTTTACACCTTTTCTACTGT
ACACCCCATCCAGACGAAGACAGTCCCTGGATCACCGACAGCACAGACAGAATCCCTCGTACCAATATGGACTCCAGTCATAGTA
CAACGCTTCAGCCTACTGCAATCCAACACAGGTTTGGTGGAAGATTGGACAGGACAGGACCTCTTCAATGACAACGCAGCAG
AGTAATTCTCAGAGCTTCTCTACATCACATGAAGGCTTGGAGAAGATAAAGACCATCCAACAACCTTCTACTCTGACATCAAGCAA
TAGGAATGATGTCACAGGTGGAAGAAGAGACCCAAATCATTCTGAAGGCTCAACTCATTTACTGGAAGGTTATACCTCTCATTACC
CACACACGAAGGAAAGCAGGACCTTCATCCAGTGACCTCAGCTAAGACTGGGTCCTTTGGAGTTACTGCAGTTACTGTTGGAGAT
TCCAACCTCTAATGTCAATCGTTCCTTATCAGGAGACCAAGACACATTCCACCCCACTGGGGGGTCCCATACCACTCATGGATCTGA
ATCAGATGGACACTCACATGGGAGTCAAGAAGGTGGAGCAAACAACCTCTGGTCCTATAAGGACACCCCAATTCAGAAATGGC
TGATCATCTTGGCATCCCTCTTGGCCTTGGCTTTGATTCTTGCAGTTTGCATTGCAGTCAACAGTCAAGAAGGTGTGGGCAGAAG
AAAAAGCTAGTGATCAACAGTGGCAATGGAGCTGTGGAGGACAGAAAGCCAAGTGGACTCAACGGAGAGGCCAGCAAGTCTCAGGA
AATGGTGCAATTGGTGAACAAGGAGTCGTGAGAACTCCAGACCAGTTTATGACAGCTGATGAGACAAGGAACCTGCAGAATGTGG
ACATGAAGATTGGGGTGTAA

FIG. 18A

MDKFWHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEADLCKAFNSTLPTMAQMEKALSIGFETCRYGFIEGHV
VIPRIHPNSICAANNTGVYILTYNTSQYDTYCFNASAPPEEDCTSVTDLNPAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSN
PTDDDVSSGSSSERSSTSGGYIFYTFSTVHPIPEDDSPWITDSTDRIPTNMDSSHSTTLQPTANPNTGLVEDLDRTGPLSMTTQ
SNSQSFSTSHGLEEDKDHPTTSTLTSSNRNDVTGRRDPNHSEGSTHLLGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGD
SNSNVNRSLSGDQDTFHPSGGSHTHGSESDGHSQEGGANTTSGPIRTPQIPEWLIILASLLALALILAVCIAVNSRRRCGQK
KKLVINSNGNAVEDRKPSSGLNGEASKSQEMVHLVNKESSETPDQFMTADETRNLQNVDMKIGV

FIG. 18B

CTTTGATGAGCACTAGTGCTACAGCAACTGAGACAGCAACCAAGAGGCAAGAAGCCTGGGATTGGTTTTTCATGGTTGTTTCTACCA
TCAGAGTCAAAGAATCATCTTCACACAACAACACAAATGGCTG

FIG. 19A

GTACGTCTTCAAATACCATCTCAGCAGGCTGGGAGCCAAATGAAGAAAATGAAGATGAAAGAGACAGACACCTCAGTTTTTCTGGA
TCAGGCATTGATGATGATGAAGATTTTATCTCCAGCACCA

FIG. 19B

TTTCAACCACACCACGGGCCTTTGACCACACAAAACAGAACCAGGACTGGACCCAGTGGAAACCAAGCCATTCAAATCCGGAAGTG
CTACTTCAGACAACCACAAGGATGACTG

FIG. 19C

ATGTAGACAGAAATGGCACCCTGCTTATGAAGGAACTGGAACCCAGAAGCACACCCTCCCCTCATTACCATGAGCATCATGAG
GAAGAAGAGACCCACATTCTACAAGCACAA

FIG. 19D

TCCAGGCAACTCCTAGTAGTACAACGGAAGAAACAGCTACCCAGAAGGAACAGTGGTTTGGCAACAGATGGCATGAGGGATATCGC
CAAACACCCAGAGAAGACTCCCATTCGACAACAGGGACAGCTG

FIG. 19E

CAGCCTCAGCTCATACCAGCCATCCAATGCAAGGAAGGACAACACCAAGCCCAGAGGACAGTTCCTGGACTGATTTCTTCAACCCA
ATCTCACACCCCATGGGACGAGGTCATCAAGCAGGAAGAAGGATGG

FIG. 19F

ATATGGACTCCAGTCATAGTACAACGCTTCAGCCTACTGCAAATCCAAACACAGGTTTGGTGGAAAATTGGACAGGACAGGACCT
CTTTCAATGACAACGC

FIG. 19G

AGCAGAGTAATTCTCAGAGCTTCTCTACATCACATGAAGGCTTGAAGAAGATAAAGACCATCCAACAACCTTCTACTCTGACATCA
AGCA

FIG. 19H

ATAGGAATGATGTCACAGGTGGAAGAAGAGACCCAAATCATTCTGAAGGCTCAACTACTTTACTGGAAGGTTATACCTCTCATTAC
CCACACACGAAGGAAAGCAGGACCTTCATCCAGTGACCTCAGCTAAGACTGGGTCCTTGGAGTTACTGCAGTTACTGTTGGAGA
TTCCAACCTCTAATGTCAATCGTTCCTTATCAG

FIG. 19I

Sequences of GPR49**A) Nucleic sequence GPR49 mRNA sequence:**

>gi|4504378|ref|NM_003667.1| Homo sapiens G protein-coupled receptor 49 (GPR49), mRNA
ATGGACACCTCCCGGCTCGGTGTGCTCCTGTCCCTGCCTGTGCTGCTGCAGCTGGCGACCGGGGGCAGCTC
TCCAGGTCTGGTGTGTGCTGAGGGGCTGCCCCACACACTGTCATTGCGAGCCCGACGGCAGGATGTTGC
TCAGGGTGGACTGCTCCGACCTGGGGCTCTCGAGCTGCCTTCCAACCTCAGCGTCTTACCTCCTACCTA
GACCTCAGTATGAACAACATCAGTCAGCTGCTCCCGAATCCCTGCCAGTCTCCGCTTCTGGAGGAGTT
ACGTCTTGCGGGAAACGCTCTGACATACATTCCCAAGGGAGCATTCACTGGCCTTTACAGTCTTAAAGTTC
TTATGCTGCAGAATAATCAGCTAAGACACGTACCCACAGAAGCTCTGCAGAATTTGCGAAGCCTTCAATCC
CTGCGTCTGGATGCTAACCACATCAGCTATGTGCCCCAAGCTGTTTCAGTGGCCTGCATTCCTTGAGGCA
CCTGTGGCTGGATGACAATGCGTTAACAGAAATCCCCGTCAGGCTTTTAGAAGTTTATCGGCATTGCAAG
CCATGACCTTGCCCTGAACAAAATACACCACATACCAGACTATGCCTTTGGAAACCTCTCCAGCTTGGTA
GTTCTACATCTCCATAACAATAGAATCCACTCCCTGGGAAAGAAATGCTTTGATGGGCTCCACAGCCTAGA
GACTTTAGATTTAAATTACAATAACCTTGATGAATTCCCCACTGCAATTAGGACACTCTCCAACTTAAAG
AACTAGGATTTTCATAGCAACAATATCAGGTCGATACCTGAGAAAGCATTGTAGGCAACCCCTCTCTTATT
ACAATACATTTCTATGACAATCCCATCCAATTTGTGGGAGATCTGCTTTTCAACATTTACCTGAACTAAG
AACACTGACTCTGAATGGTGCCTCACAATAACTGAAATTCCTGATTTAACTGGAAGTGCACAACTGGAGA
GTCTGACTTTAACTGGAGCACAGATCTCATCTCTTCCCTCAAACCGTCTGCAATCAGTTACCTAATCTCCAA
GTGCTAGATCTGTCTTACAACCTATTAGAAGATTTACCCAGTTTTTCAGTCTGCCAAAAGCTTCAGAAAAT
TGACCTAAGACATAATGAAATCTACGAAATTAAGTTGACACTTTCCAGCAGTTGCTTAGCCTCCGATCGC
TGAATTTGGCTTGGAACAAAATTGCTATTATTACCCCAATGCATTTTCCACTTTGCCATCCCTAATAAAG
CTGGACCTATCGTCCAACCTCCTGTGCTCTTTTCCCTATAACTGGGTTACATGGTTTAACTCACTTAAATTT
AACAGGAAATCATGCCCTTACAGAGCTTGATATCATCTGAAAACTTCCAGAACTCAAGGTTATAGAAATGC
CTTATGCTTACCAGTGTGTGCATTTGGAGTGTGTGAGAATGCCATATAAGATTTCTAATCAATGGAATAAA
GGTGACAACAGCAGTATGGACGACCTTCATAAGAAAGATGCTGGAATGTTTCAGGCTCAAGATGAACGTGA
CCTTGAAGATTTCCCTGCTTGACTTTGAGGAAGACCTGAAAGCCCTTCATTCAGTGCAGTGTTCACCTTCCC
CAGGCCCCCTTCAAACCCGTGTAACACCTGCTTGATGGCTGGCTGATCAGAATTGGAGTGTGGACCATAGCA
GTTCTGGCACTTACTTGTAAATGCTTTGGTGACTTCAACAGTTTTCAGATCCCTCTGTACATTTCCCCCAT
TAAAGTGTAAATTGGGGTTCATCGCAGCAGTGAACATGCTCACGGGAGTCTCCAGTGCCGTGCTGGCTGGTG
TGGATGCGTTTCACTTTTGGCAGCTTTGCACGACATGGTGCCCTGGTGGGAGAATGGGGTTGGTTGCCATGTC
ATTGGTTTTTTGTCCATTTTGTCTTCAAGATCATCTGTTTTCTGCTTACTCTGGCAGCCCTGGAGCGTGG
GTTCTCTGTGAAATATTTCTGCAAAATTTGAAACGAAAGCTCCATTTTCTAGCCTGAAAGTAATCATTTTGC
TCTGTGCCCTGCTGGCCTTGACCATGGCCGAGTTCCCCCTGCTGGGTGGCAGCAAGTATGGCGCCTCCCCCT
CTCTGCCCTGCCCTTTGCCCTTTGGGGAGCCCAGCACCATGGGCTACATGGTCTGCTCTCATCTTGCTCAATTC
CCTTTGCTTCCCTCATGATGACCATTGCCCTACACCAAGCTCTACTGCAATTTGGACAAGGGAGACCTGGAGA
ATATTTGGGACTGCTCTATGGTAAACACATTGCCCTGTTGCTCTTACCAACTGCATCCTAAACTGCCCT
GTGGCTTTCTTGCTCTTCTCCTCTTTAATAAACCTTACATTTATCAGTCTTGAAGTAATTAAGTTTATCCT
TCTGGTGGTAGTCCCACTTCCCTGCATGTCTCAATCCCCTTCTCTACATCTTGTTCATCTCACTTTAAGG
AGGATCTGGTGAGCTTGAGAAAGCAAACCTACGTCTGGACAAGATCAAAACACCCAGCTTGTATGTCAATT
AAGTCTGATGATGTCGAAAAACAGTCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGCTCCAGCAT
CACTTATGACCTGCCTCCAGTTCCGTGCCATACCAGCTTATCCAGTGACTGAGAGCTGCCATCTTTCCT
CTGTGGCATTGTGCCATGTCTCTAA (SEQ ID No. 3)

FIG. 20A

B) Proteic sequence

>gi|4504379|ref|NP_003658.1| (NM_003667) G protein-coupled receptor
49; G protein-coupled receptor 67; orphan G protein-coupled receptor
HG38 [Homo sapiens]
MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPHCHCEPDGRMLLRVDCSDLGLSELPSNLSVFTS
YLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYPKGAFTGLYSLKVLMLQNNQLRHVPTEALQNL
SLQSLRLDANHISYVPPSCFSGHSLRHLWLDNLTALTEIPVQAFRSLALQAMTLALNKIHHIPDYAFG
NLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLDLNNNNLDEFPTAIRTLNLKELGFHSNNIRSIPKA
FVGNPSLITIHFDNPIQFVGRSAFQHLPELRTLTLNGASQITEFPDLTGANLESLLTGAQISSLPQ
TVCNQLPNLQVLDLSYNLLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSLRSNLAWNKIAI
H PNAFSTLPSLIKLDLSSNLLSSFPITGLHGLTHLKLGTGNHALQSLISSENFPELKVIEMPYAYQCCAFG
VCENAYKISNQWNKGDNSMDDLHKKDAGMFQAQDERDLEDFLDFFEDLKALHSVQCSPSPGPFKPCE
HLLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYISPIKLLIGVIAAVNMLTGVS
SAVLAVLAGVDAFTF GSFARHGAWWENGVGCHVIGFLSIFASESSVFLTLAALERGF
SVKYSAKFETKAPFSSLKVIILLCAL LALTMAAVPLLGGSKYGASPLCLPLPFGE
PSTMGYMVALILLNSLCFLMMTIAYTKLYCNLDKGDLENI WDCSMVKHIALLLFTNCILNCPVAF
LSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLYILFNPHFK EDLVSLRKQTYVWTRSKHPS
LMSINSDDVEKQSCDSTQALVTFTSSSITYDLPPSSVPSPAYPVTESCH LSSVAFVPCL (SEQ ID No.4)

FIG. 20B

EPHB4 sequence:

A) Nucleic sequence

>gi|17975769|ref|NM_004444.2| Homo sapiens EphB4 (EPHB4), mRNA

CGTCCACCCGCCAGGGAGAGTCAGACCTGGGGGGGCGAGGGCCCCCAAACCTCAGT
TCGGATCCTACCCGAGTGAGGCGGCGCCATGGAGCTCCGGGTGCTGCTCTGCTGGGC
TTCGTTGGCCGCAGCTTTGGAAGAGACCCCTGCTGAACACAAAATTGGAAACTGCTGA
TCTGAAGTGGGTGACATTCCTCAGGTGGACGGGCAGTGGGAGGAACTGAGCGGCCT
GGATGAGGAACAGCACAGCGTGCGCACCTACGAAGTGTGTGAAGTGCAGCGTGCCCC
GGGCCAGGCCACTGGCTTCGCACAGGTTGGGTCCCACGGCGGGGCGCCGTCCACGT
GTACGCCACGCTGCGCTTCACCATGCTCGAGTGCCTGTCCCTGCCTCGGGCTGGGCG
CTCCTGCAAGGAGACCTTCACCGTCTTCTACTATGAGAGCGATGCGGACACGGCCAC
GGCCCTCACGCCAGCCTGGATGGAGAACCCCTACATCAAGGTGGACACGGTGGCCGC
GGAGCATCTCACCCGGAAGCGCCCTGGGGCCGAGGCCACCGGGAAGGTGAATGTCAA
GACGCTGCGTCTGGGACCGCTCAGCAAGGCTGGCTTCTACCTGGCCTTCCAGGACCA
GGGTGCCTGCATGGCCCTGCTATCCCTGCACCTCTTCTACAAAAGTGCGCCAGCT
GACTGTGAACCTGACTCGATTCCCGGAGACTGTGCCTCGGGAGCTGGTTGTGCCCGT
GGCCGGTAGCTGCGTGGTGGATGCCGTCCCCGCCCTGGCCCCAGCCCCAGCCTCTA
CTGCCGTGAGGATGGCCAGTGGGCCGAACAGCCGGTCACGGGCTGCAGCTGTGCTCC
GGGGTTTCGAGGCAGCTGAGGGGAACACCAAGTGCCGAGCCTGTGCCAGGGCACCTT
CAAGCCCCCTGTGAGGAGAAGGGTCCTGCCAGCCATGCCAGCCAATAGCCACTCTAA
CACCATTGGATCAGCCGTCTGCCAGTGCCGCGTCGGGTACTTCCGGGCACGCACAGA
CCCCCGGGGTGCACCCTGCACCACCCCTCCTTCGGCTCCGCGGAGCGTGGTTTCCCG
CCTGAACGGCTCCTCCCTGCACCTGGAATGGAGTGCCCCCTGGAGTCTGGTGGCCG
AGAGGACCTCACCTACGCCCTCCGCTGCCGGGAGTGCCGACCCGGAGGCTCCTGTGC
GCCCTGCGGGGGAGACCTGACTTTTGACCCCGGCCCGGGACCTGGTGGAGCCCTG
GGTGGTGGTTCGAGGGCTACGTCCGGACTTCACCTATACCTTTGAGGTCACTGCATT
GAACGGGGTATCCTCCTTAGCCACGGGGCCCGTCCCATTGAGCCTGTCAATGTCAC
CACTGACCGAGAGGTACCTCCTGCAGTGTCTGACATCCGGGTGACGCGGTCTCACC
CAGCAGCTTGAGCCTGGCCTGGGCTGTTCCCCGGGCACCCAGTGGGGCGTGGCTGGA
CTACGAGGTCAAATACCATGAGAAGGGCGCCGAGGGTCCCAGCAGCGTGCGGTTCCCT
GAAGACGTGAGAAAACCGGGCAGAGCTGCGGGGGCTGAAGCGGGGAGCCAGCTACCT
GGTGCAGGTACGGGCGCGCTCTGAGGCCGGCTACGGGCCCTTCGGCCAGGAACATCA
CAGCCAGACCCAACCTGGATGAGAGCGAGGGCTGGCGGGAGCAGCTGGCCCTGATTGC
GGGCACGGCAGTCGTGGGTGTGGTCTGGTCTGGTGGTTCATTGTGGTTCGAGTTCT
CTGCCTCAGGAAGCAGAGCAATGGGAGAGAAGCAGAATATTCGGACAAACACGGACA
GTATCTCATCGGACATGGTACTAAGGTCTACATCGACCCCTTCACTTATGAAGACCC
TAATGAGGCTGTGAGGGAATTTGCAAAAGAGATCGATGTCTCCTACGTCAAGATTGA
AGAGGTGATTGGTGCAGGTGAGTTTGGCGAGGTGTGCCGGGGGCGGCTCAAGGCCCC
AGGGAAGAAGGAGAGCTGTGTGGCAATCAAGACCCTGAAGGGTGGCTACACGGAGCG
GCAGCGGCGTGAGTTTCTGAGCGAGGCCTCCATCATGGGCCAGTTCGAGCACCCCAA
TATCATCCGCCTGGAGGGCGTGGTCAACACAGCATGCCCGTCATGATTCTCACAGA
GTTTCATGGAGAACGGCGCCCTGGACTCCTTCCCTGCGGCTAAACGACGGACAGTTTAC
AGTCATCCAGCTCGTGGGCATGCTGCGGGGCATCGCCTCGGGCATGCGGTACCTTGC
CGAGATGAGCTACGTCCACCGAGACCTGGCTGCTCGCAACATCCTAGTCAACAGCAA

FIG. 21A

CCTCGTCTGCAAAGTGTCTGACTTTGGCCTTTCCCGATTCTTGAGGAGAACTCTTC
CGATCCCACCTACACGAGCTCCCTGGGAGGAAAGATTCCCATCCGATGGACTGCCCC
GGAGGCCATTGCCTTCCGGAAGTTCACTTCCGCCAGTGATGCCTGGAGTTACGGGAT
TGTGATGTGGGAGGTGATGTCATTTGGGGAGAGGCCGTACTGGGACATGAGCAATCA
GGACGTGATCAATGCCATTGAACAGGACTACCGGCTGCCCCCGCCCCAGACTGTCC
CACCTCCCTCCACCAGCTCATGCTGGACTGTTGGCAGAAAGACCGGAATGCCCGGCC
CCGCTTCCCCCAGGTGGTCAGCGCCCTGGACAAGATGATCCGGAACCCCGCCAGCCT
CAAAATCGTGGCCCGGGAGAATGGCGGGGCCTCACACCCTCTCCTGGACCAGCGGCA
GCCTCACTACTCAGCTTTTGGCTCTGTGGGCGAGTGGCTTCGGGGCCATCAAAATGGG
AAGATACGAAGAAAGTTTCGCAGCCGCTGGCTTTGGCTCCTTCGAGCTGGTCAGCCA
GATCTCTGCTGAGGACCTGCTCCGAATCGGAGTCACTCTGGCGGGACACCAGAAGAA
AATCTTGGCCAGTGTCCAGCACATGAAGTCCCAGGCCAAGCCGGGACCCCGGGTGGG
ACAGGAGGACCGGCCCGCAGTACTGACCTGCAGGAACTCCCCACCCAGGGACACC
GCCTCCCCATTTTCCGGGGCAGAGTGGGGACTCACAGAGGCCCCCAGCCCTGTGCCC
CGCTGGATTGCACTTTGAGCCCGTGGGGTGAGGAGTTGGCAATTTGGAGAGACAGGA
TTTGGGGGTTCTGCCATAATAGGAGGGGAAAATCACCCCCAGCCACCTCGGGGAAC
TCCAGACCAAGGGTGAGGGCGCCTTTCCTCAGGACTGGGTGTGACCAGAGGAAAAG
GAAGTGCCCAACATCTCCAGCCTCCCCAGGTGCCCCCCTCACCTTGATGGGTGCGT
TCCCGCAGACCAAAGAGAGTGTGACTCCCTTGCCAGCTCCAGAGTGGGGGGGCTGTC
CCAGGGGGCAAGAAGGGGTGTGAGGGCCAGTGACAAAATCATTGGGGTTTGTAGTC
CCAACCTTGCTGCTGTCACCACCAAACCTCAATCATTTTTTTCCCTTGTAATGCCCT
CCCCCAGCTGCTGCCTTCATATTGAAGGTTTTTGAGTTTTGTTTTTGGTCTTAATTT
TTCTCCCCGTTCCCTTTTTGTTTTCTTCGTTTTGTTTTTCTACCGTCCTTGTCATAAC
TTTGTGTTGGAGGGAACCTGTTTCACTATGGCCTCCTTTGCCCAAGTTGAAACAGGG
GCCCATCATCATGTCTGTTTCCAGAACAGTGCCTTGGTCATCCCACATCCCCGACC
CCGCTGGGACCCCCAAGCTGTGTCCTATGAAGGGGTGTGGGGTGAGGTAGTGAAAA
GGGCGGTAGTTGGTGGTGGAACCCAGAAACGGACGCCGGTGCTTGAGGGGGTTCTTA
AATTATATTTAAAAAGTAACTTTTTGTATAAATAAAAGAAAATGGGACGTGTCCCA
GCTCCAGGGGT (SEQ ID No.5)

FIG. 21B

B) Proteic sequence

>gi|17975770|ref|NP_004435.2| (NM_004444) ephrin receptor EphB4 precursor. Ephrin receptor EphB4 (hepatoma transmembrane kinase); Tyroll; ephrin receptor EphB4; hepatoma transmembrane kinase [Homo sapiens]

MELRVLLCWASLAAALEETLLNNTKLETADLKWVTFPQVDGQWEELSGLDEEQHSVRTYEVCEVQRAPGQAH
WLRTGWVPRRGAVHVYATLRFTMLECLSLPRAGRSCKETFTVFYYESDADTATALTPAWMENPYIKVDTVA
AEHLTRKRPGAEATGKVVNKTLLRLGPLSKAGFYLAFAQDQGACMALLSLHLFYKKCAQLTVNLTRFPETVPR
ELVVPVAGSCVVDAPVAPGPSPLYCREDGQWAEQPVGTGSCAPGFEEAEGNTKCRACAQGTFFKPLSGEGS
CQPCPANSHTIGSAVCQCRVGYFRARTDPRGAPCTTPPSAPRSVVSRLNGSSLHLEWSAPLES GGREDL
TYALRCRECRPGGSCAPCGGDLTFDPGPRDLVEPWVVVRGLRPDFTYTFEVTALNGVSSLATGPVPFEPVN
VTTDREVPPAVSDIRVTRSSPSSLSLAWAVPRAPSGAWLDYEVKYHEKGAEGPSSVRFLKTSENRAELRGL
KRGASYLVQVRARSEAGYGPFQGEHHSQTQLDESEGWREQLALIAGTAVVGVLVLVVIWVAVLCLRKQSN
GREAEYS DKHGQYLIGHGTKVYIDPFTYEDPNEAVREFAKEIDVS YVKIEEVIGAGEFGEVCRGRLKAPGK
KESCVAIKTLKGGYTERQRREFLSEASIMGQFEHPNIIRLEGVVTNSMPVMILTEFMENGALDSFLRLNDG
QFTVIQLVGMLRGIASGMRYLAEMSYVHRDLAARNILVNSNLVCKVSDFGLSRFLEENSSDPTYTSSLGK
IPIRWTAPEAIAFRKFTSASDAWSYGIVMWEVMSFGERPYWDMSNQDVINAIEQDYRLPPPPDCPTSLHQL
MLDCWQKDRNARPRFPQVVSALDKMIRNPASLKIVARENGGASHPLLDQRQPHYSAFGSVGEWLRAIKMGR
YEESFAAAGFGSFELVSQISAEDLLRIGVTLAGHQKKILASVQHMKSQAKPGTPGGTGGPAPQY (SEQ
ID No.6)

FIG. 21C

GPX2 Sequence**A) Nucleic sequence**

>gi|4504102|ref|NM_002083.1| Homo sapiens glutathione peroxidase 2
(gastrointestinal) (GPX2), mRNA

CGGCCTCTCTGCGGGGCTCACTCTGCGCTTCACCATGGCTTTCATTGCCAAGTCCTT
CTATGACCTCAGTGCCATCAGCCTGGATGGGGAGAAGGTAGATTTCAATACGTTCCG
GGGCAGGGCCGTGCTGATTGAGAATGTGGCTTCGCTCTGAGGCACAACCACCCGGGA
CTTCACCCAGCTCAACGAGCTGCAATGCCGCTTCCCAGGCGCCTGGTGGTCCTTGG
CTTCCCTTGCAACCAATTTGGACATCAGGAGAACTGTCAGAATGAGGAGATCCTGAA
CAGTCTCAAGTATGTCCGTCCTGGGGGTGGATAACCAGCCACCTTCACCCTTGTTCA
AAAATGTGAGGTGAATGGGCAGAACGAGCATCCTGTCTTCGCCTACCTGAAGGACAA
GCTCCCCCTACCCTTATGATGACCCATTTTCCCTCATGACCGATCCCAAGCTCATCAT
TTGGAGCCCTGTGCGCCGCTCAGATGTGGCCTGGAACCTTTGAGAAAGTTCCCTCATAGG
GCCGGAGGGAGAGCCCTTCCGACGCTACAGCCGCACCTTCCCAACCATCAACATTGA
GCCTGACATCAAGCGCCTCCTTAAAGTTGCCATATAGATGTGAACTGCTCAACACAC
AGATCTCCTACTCCATCCAGTCCTGAGGAGCCTTAGGATGCAGCATGCCTTCAGGAG
ACACTGCTGGACCTCAGCATTCCTTGATATCAGTCCCCTTCACTGCAGAGCCTTGC
CTTTCCCCTCTGCCTGTTTCCTTTTCTCTCCCAACCCTCTGGTTGGTGATTCAACT
TGGGCTCCAAGACTTGGGTAAGCTCTGGGCCTTCACAGAATGATGGCACCTTCCTAA
ACCCTCATGGGTGGTGTCTGAGAGGCGTGAAGGGCCTGGAGCCACTCTGCTAGAAGA
GACCAATAAAGGGCAGGTGTGGAAACGGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA (SEQ ID No.7)

FIG. 22A**B) GPX2 Protein Sequence:**

>gi|4504103|ref|NP_002074.1| gastrointestinal glutathione peroxidase
2 [Homo sapiens]

MAFIAKSFYDLAISLDGEKVDENTFRGRAVLIENTVASLXGTTTTRDFTQLNELQCRF
PRRLVVLGFPCNQFGHQENCQNEEILNSLKYVRPGGGYQPTFTLVQKCEVNGQNEHP
VFAYLKDKLPYPYDDPFSLMTDPKLIWSPVRRSDVAWNFEKFLIGPEGEPFRRYSR
TFPTINIEPDIKRLKVAI (SEQ ID No.8)

FIG. 22B

Sequences of Tspan 5:**A) Nucleic sequence**

>gi|21264582|ref|NM_005723.2| Homo sapiens tetraspan 5 (TM4SF9), mRNA
CGCCTTTGCCCGAAGCCCGGGGACGAACCGACGGACCGACCGCCTGGCGCACGGACGCGGGCGCTCGCT
TTGTGTTCCGGGGCTAGCGTCGGCGAGGCTTGAGCTTGACGCGCGCGGCTTCCCTGCTTTCTCGCGGCCA
CCCCGGCTCCGGCGGCCTCGGCGCGCGAGGGGCTGGAGGTGCGGGAGCCGCTCTCCGCCGGTCGGTCCC
CGCGCGGCTGAGCCCAGGCCGCCAGCGCCGCGGGCCCCGTGCGGTGTCCCTGAGCTCCTGCTCCCCGCCG
GGCTGCTCCGAGCAACGGTGCTTCGGAGCTCCAACTCGGGCTGCCGGGGCAAGTGTCTTCATGAACCC
AGAGGATGTCCGGGAAGCACTACAAGGGTCTGAAGTCAGTTGTTGCATCAAATACTTCATATTTGGCT
TCAATGTCATATTTTGGTTTTTGGGAATAACATTTCTTGGAATTGGACTGTGGGCATGGAATGAAAAAG
GAGTTCTGTCCAACATCTCTTCCATCACCGATCTCGGCGGCTTTGACCCAGTTTGGCTCTTCCTTGTTG
TGGGAGGAGTGATGTTTCAATTTTGGGATTTGCAGGGTGCATTGGAGCGCTACGGGAAAACACTTTCCTTC
TCAAGTTTTTTTTCTGTGTTTCTGGGAATTATTTTCTTCTGAGCTCACTGCCGGAGTTCTAGCATTTG
TTTTCAAAGACTGGATCAAAGACCAGCTGTATTTCTTTATAAACAACAACATCAGAGCATATCGGGATG
ACATTGATTTGCAAAACCTCATAGACTTCACCCAGGAATATTGGCAGTGCTGTGGGGCTTTTGGAGCTG
ATGATTGGAACCTAAATATTTACTTCAATTGCACAGATTCCAATGCAAGTCGAGAGCGATGTGGCGTTC
CATTCTCCTGCTGCACTAAAGATCCCGCAGAAGATGTCATCAACACTCAGTGTGGCTATGATGCCAGGC
AAAAACCAGAAGTTGACCAGCAGATTGTAATCTACACGAAAGGCTGTGTGCCCCAGTTTGAGAAGTGGT
TGCAGGACAATTTAACCATCGTTGCTGGTATTTTCATAGGCATTGCATTGCTGCAGATATTTGGGATAT
GCCTGGCCCAGAATTTGGTTAGCGATATCGAAGCTGTCAGGGCGAGCTGGTAGACCCCCTGCAACCGCT
GCTGCAAGACACTGGACAGACCCAGCTTTCGGGACCCCTCCCGCGTGCCGAAGTATCTTCGAGCTGCAT
GGACCTAATCACAGATGCAGCCTGCAGTCTCGCCTAATGGAGCTGCCATTAGGGGAGTGTAAGTGGG
AAATGCTGCTCACTGACAGAATTAATAAAAAAAAAAATAACCAGTATGAAAGTCGTTGCGCCGTGAATCTCT
ACTGTAGCCATGAATTTATGGACAGTTAGATGCTTACCAAAAAAGAAAAAAA (SEQ ID No.11)

FIG. 24A**B) Protein Sequence of Tspan5:**

>gi|21264583|ref|NP_005714.2| (NM_005723) tetraspan 5; tetraspan
TM4SF; tetraspan NET-4; transmembrane 4 superfamily member 9;
transmembrane 4 superfamily, member 8; tetraspanin 5 [Homo sapiens]
MSGKHYKGPEVSCCIKYFIFGFNVIFWFLGITFLGIGLWAWNEKGVLSNISSITDLGGFDPVWLFLVVG
GVMFILGFAGCIGALRENTFLKFFSVFLGIIFLELTAGVLAFFVKDWIKDQLYFFINNNIRAYRDDI
DLQNLIDFTQEYWQCCGAFGADDWNLNIYFNCTDSNASRERCGVPFSCCTKDPADVINTQCGYDARQK
PEVDQQIVIIYTKGCVPPQFEKWLQDNLTIVAGIFIGIALQLQIFGICLAQNLVSDIEAVRASW (SEQ ID
No.12)

FIG. 24B